

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:51:30 ; Search time 194 Seconds
(without alignments)
525.563 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRHHVRLFTVSLAQII.....PSVLQRRPCGRPLGHLRL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 6

Total number of hits satisfying chosen parameters: 14456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223	100.0	223	8	ADO05060 Human cri
2	223	100.0	223	4	AAU18122 Novel hum
3	223	100.0	229	4	AAU17028 Human nov
4	223	100.0	229	4	ABB10300 Human CDN
5	223	100.0	229	4	AAU19904 Novel hum
6	223	100.0	229	5	ABJ05749 Novel hum
7	223	100.0	229	5	ABP66887 Human pol
8	187	83.9	223	5	ABP90336 Human pol
9	187	83.9	223	6	ABU56711 Lung canc
10	187	83.9	223	7	ADN39104 Cancer/an
11	187	83.9	223	7	ADN39975 Cancer/an
12	187	83.9	223	9	ADY85963 Human Cri
13	187	83.9	231	4	AAU16957 Human nov
14	149	66.8	230	2	AAW09111 Human cri
15	145	65.0	223	5	AAG77914 Human cry
16	15	6.7	202	9	ADY85962 Murine Cr
17	14	6.3	14	4	AAW00665 Human pro
18	8	3.6	60	4	AAW06349 Human foe
19	8	3.6	64	4	AAW06772 Human foe
20	8	3.6	120	4	AAO10911 Human pol
21	8	3.6	158	4	ABB68713 Drosophil
22	8	3.6	180	4	AAW99763 Human exc
23	8	3.6	180	4	AAW42398 Human pol

24	8	3.6	180	4	AAW42578 Human kid
25	8	3.6	333	7	ABM86084 Rice abio
26	8	3.6	334	8	ADU02861 Novel hum
27	8	3.6	363	7	ABO69270 Pseudomon
28	8	3.6	420	6	ABU11822 Human MDD
29	8	3.6	575	8	ADY08754 Plant ful
30	8	3.6	575	8	ADY12991 Plant ful
31	8	3.6	737	8	ADY08040 Plant ful
32	8	3.6	788	8	ADO55178 Protein #
33	8	3.6	1230	5	AAO21533 Human mit
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35	8	3.6	1230	7	ADD45964 Human Pro
36	8	3.6	1253	4	ABG23851 Novel hum
37	8	3.6	1718	5	AAE26420 Human tra
38	8	3.6	2523	8	ADL26915 Xenopus s
39	7	3.1	21	9	ADV55161 G protein
40	7	3.1	22	7	ADE28537 Human CD1
41	7	3.1	24	5	ABB74254 Fusogenic
42	7	3.1	27	4	AAE03135 Human gen
43	7	3.1	30	9	ADZ77602 Human MHC
44	7	3.1	33	9	ADY28315 Novel Erb
45	7	3.1	38	4	AAO03363 Human pol

ALIGNMENTS

RESULT 1

ADO05060	ID	ADO05060 standard; protein; 223 AA.
XX	AC	ADO05060;
XX	DT	29-JUL-2004 (first entry)
XX	DE	Human criptin growth factor (CGF) protein.
XX	KW	Criptin growth factor; CGF; wound healing; tissue regeneration;
KW	KM	Implant fixation; angiogenesis; neoplasia; tumour; gene therapy; human.
XX	OS	Homo sapiens.
XX	PN	US2004086967-A1.
XX	PD	06-MAY-2004.
XX	PF	22-SEP-2003; 2003US-00665602.
XX	PR	06-JUN-1995; 95US-00471371.
XX	PR	09-SEP-1999; 99US-00393023.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Meissner PS, Coleman TA;
XX	DR	WPI; 2004-356201/33.
XX	DR	N-PSDB; ADO05059.
XX	PT	New human polynucleotides encoding human criptin growth factor
XX	PT	polypeptides, useful for wound healing or tissue regeneration,
XX	PT	stimulating implant fixation and angiogenesis, and for treating and/or
XX	PS	preventing tumor.
XX	PS	Claim 12; SEQ ID NO 2; 19pp; English.
XX	CC	The invention provides criptin growth factor (CGF) polypeptides and their
XX	CC	encoding polynucleotides. The invention is useful for wound healing and
XX	CC	tissue regeneration, stimulating implant fixation, angiogenesis and for
XX	CC	treating and preventing neoplasia such as tumour. The invention is also
XX	CC	useful in gene therapy. The present sequence is human criptin growth
XX	CC	factor (CGF) protein.
XX	SQ	Sequence 223 AA;

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ID	AAU18122 standard; protein; 229 AA.				
XX	AAU18122;				
AC					
DT	21-NOV-2001 (first entry)				
XX					
DE	Novel human uterine motility-association polypeptide #29.				
XX					
KW	Human; uterine motility-association disorder; uterus; pregnancy; labour;				
XX	menstrual cycle; gene therapy.				
OS	Homo sapiens.				
XX					
PN	W020015201-A1.				
XX					
PD	02-AUG-2001.				
XX					
PF	17-JAN-2001; 2001WO-US001317.				
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PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WFI; 2001-488777/53.
DR N-PSDB; AAS28964.
XX
XX New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
XX Claim 11; SEQ ID NO 98; 524pp; English.
XX
XX The present invention relates to the isolation of novel human uterine
CC motility-association polypeptides, and cDNA (AAS28936-AAS28994) and
CC genomic sequences encoding for these polypeptides. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with uterine motility such as pregnancy
CC and labour, and menstrual disorders. The polynucleotide sequences of the
CC invention are also useful in gene therapy. AAU18094-AAU18152 represent
CC novel human uterine motility-association polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 229 AA;
Query Match 100.0%; Score 223; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-195;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 181 LLPCALLHRLLRDPADAPAHPSLVPSVLQRRRRCGRFGLGHL 223
Db 187 LLPCALLHRLLRDPADAPAHPSLVPSVLQRRRRCGRFGLGHL 229

RESULT 3
AAU17028
ID AAU17028 standard; protein; 229 AA.
XX
AC AAU17028;
XX
DT 07-NOV-2001 (first entry)
XX
XX Human novel secreted protein, SEQ ID 269.
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; vulnery;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cerebrovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
OS Homo sapiens.
XX
XX WO200155441-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001320.
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XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
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 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476222/51.

N-PSDB; AAS26933.

Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

Claim 11; SEQ ID NO 269; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before retransplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The

Query Match 100.0%; Score 223; DB 4; Length 229;

Best Local Similarity 100.0%; Pred. No. 1.5e-195;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGVEVTKVATQKHSPLNWTSSHFGE 60

Db 7 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGVEVTKVATQKHSPLNWTSSHFGE 66

Qy	61	VTSAEGWGPPEPLPYSAFGEASAPRCRNGGTCVLGSCFVCVPAHFTGRYCEHDQRR	120	PR	01-SEP-2000;	2000US-0229287P.
				PR	01-SEP-2000;	2000US-0229343P.
Db	67	VTSAEGWGPPEPLPYSAFGEASAPRCRNGGTCVLGSCFVCVPAHFTGRYCEHDQRR	126	PR	01-SEP-2000;	2000US-0229345P.
				PR	05-SEP-2000;	2000US-0229509P.
Qy	121	SECGALSHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL	180	PR	05-SEP-2000;	2000US-0229513P.
				PR	06-SEP-2000;	2000US-0230437P.
Db	127	SECGALSHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGAPSLLL	186	PR	06-SEP-2000;	2000US-0230438P.
				PR	08-SEP-2000;	2000US-0231242P.
Qy	181	LLPCALLHRLRPDAPAHPSLVPSVLQRRRCGRPLGHLR	223	PR	08-SEP-2000;	2000US-0231243P.
				PR	08-SEP-2000;	2000US-0231244P.
Db	187	LLPCALLHRLRPDAPAHPSLVPSVLQRRRCGRPLGHLR	229	PR	08-SEP-2000;	2000US-0231413P.
				PR	08-SEP-2000;	2000US-0231414P.
RESULT 4						
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XX	AC			PR	14-SEP-2000;	2000US-0232399P.
DT	10-JAN-2002	(first entry)		PR	14-SEP-2000;	2000US-0232400P.
XX	Human cDNA	SEQ ID NO: 608.		PR	14-SEP-2000;	2000US-0232401P.
XX				PR	14-SEP-2000;	2000US-0233063P.
KW	Human;	gene therapy; neural disorder; immune system disorder;		PR	14-SEP-2000;	2000US-0233065P.
KW	muscular disorder;	reproductive disorder; gastrointestinal disorder;		PR	21-SEP-2000;	2000US-0234223P.
KW	pulmonary disorder;	cardiovascular disorder; renal disorder;		PR	21-SEP-2000;	2000US-0234274P.
KW	proliferative disorder; inflammation.			PR	25-SEP-2000;	2000US-0234997P.
XX				PR	25-SEP-2000;	2000US-0234988P.
OS	Homo sapiens.			PR	26-SEP-2000;	2000US-0235484P.
XX				PR	27-SEP-2000;	2000US-0235834P.
PN	WO200154474-A2.			PR	27-SEP-2000;	2000US-0235836P.
XX				PR	29-SEP-2000;	2000US-0236327P.
XX				PR	29-SEP-2000;	2000US-0236367P.
PD	02-AUG-2001.			PR	29-SEP-2000;	2000US-0236368P.
				PR	29-SEP-2000;	2000US-0236369P.
XX	17-JAN-2001;	2001WO-US001349.		PR	02-OCT-2000;	2000US-0236370P.
XX				PR	02-OCT-2000;	2000US-0237037P.
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PR	18-APR-2000;	2000US-0198123P.		PR	20-OCT-2000;	2000US-0241221P.
PR	19-MAY-2000;	2000US-0205515P.		PR	20-OCT-2000;	2000US-0241785P.
PR	07-JUN-2000;	2000US-0209467P.		PR	20-OCT-2000;	2000US-0241786P.
PR	28-JUN-2000;	2000US-0214886P.		PR	20-OCT-2000;	2000US-0241787P.
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PR	26-JUL-2000;	2000US-0230964P.		PR	08-NOV-2000;	2000US-0246477P.
PR	14-AUG-2000;	2000US-0224518P.		PR	08-NOV-2000;	2000US-0246478P.
PR	14-AUG-2000;	2000US-0224519P.		PR	08-NOV-2000;	2000US-0246523P.
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PR	14-AUG-2000;	2000US-0225268P.		PR	08-NOV-2000;	2000US-0246528P.
PR	14-AUG-2000;	2000US-0225270P.		PR	08-NOV-2000;	2000US-0246532P.
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PR	14-AUG-2000;	2000US-0225758P.		PR	08-NOV-2000;	2000US-0246611P.
PR	18-AUG-2000;	2000US-0225759P.		PR	08-NOV-2000;	2000US-0246613P.
PR	18-AUG-2000;	2000US-0226279P.		PR	17-NOV-2000;	2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249300P.
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PR 05-DEC-2000; 2000US-0251988P.
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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
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PR 08-DEC-2000; 2000US-0251999P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476161/51.
XX N-PSDB; ABA06522.
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition.
XX
XX Claim 11; SEQ ID NO 608; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention
XX
XX Sequence 229 AA;
XX
XX Query Match 100.0%; Score 223; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. NO. 1.5e-195;
XX Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTRHHVRLFTVSLAQIINLNGSYOREKHNGRGVTKVATQKHQSPLNWTSFHGE 60
DB 7 MTRHHVRLFTVSLAQIINLNGSYOREKHNGRGVTKVATQKHQSPLNWTSFHGE 66
QY 61 VTGAEGWGPEEPLPYSRAFEGASAPRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 120
DB 67 VTGAEGWGPEEPLPYSRAFEGASAPRCRNGGTCVLGSCFVCVCPAHFTGRYCEHDQRR 126
QY 121 SECCALEHGAWTTRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGASLLL 180
DB 127 SECCALEHGAWTTRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGFSAGASLLL 186
QY 181 LLPCALLHRLRPDAPAHPSLVPSVLQRRRCPCRGRLGHLR 223
DB 187 LLPCALLHRLRPDAPAHPSLVPSVLQRRRCPCRGRLGHLR 229
XX
XX RESULT 5
XX AAU19904
XX ID AAU19904 standard; protein; 229 AA.
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XX AC AAU19904;
XX DT 06-DEC-2001 (first entry)
XX DE Novel human calcium-binding protein #13.
XX KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide.
XX OS Homo sapiens.
XX PN WO200155304-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001302.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
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PR 28-JUN-2000; 2000US-0214886P.
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PR 12-SEP-2000; 2000US-0231968P.

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PR 08-NOV-2000; 2000US-0246524P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.
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PR 08-DEC-2000; 2000US-0251856P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-455568/50.
XX N-PSDB; AAS31589.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; SEQ ID NO 101; 542pp; English.
XX
XX The present invention relates to the isolation of novel human calcium-
XX binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences
XX encoding for these proteins. The sequences of the invention are useful in
XX the diagnosis, prevention and/or prognosis of diseases associated with
XX aberrant calcium flux. Such disorders include neurological diseases (e.g.
XX amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe
XX combined immunodeficiency, SCID), digestive disorders (e.g. irritable
XX bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders
XX (e.g. haemophilia), and/or infectious disease (e.g. acquired
XX immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are
XX also useful as screening tools to identify antagonists and/or agonists
XX that may enhance or inhibit activities mediated by calcium-binding
XX proteins. The polynucleotides of the invention are also useful in gene
XX therapy. AAU19892-AAU19969 represent the novel human calcium-binding
XX proteins. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 229 AA;
XX
XX Query Match 100.0%; Score 223; DB 4; Length 229;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-195; Indels 0; Gaps 0;
XX Matches 223; Conservative 0; Mismatches 0;
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XX Qy 1 MTRHVRLLFTVSLALQIINLGNISYQREKHNGRGVTKVATQKHROSPLNWTSSHFGE 60
XX Db 7 MTRHVRLLFTVSLALQIINLGNISYQREKHNGRGVTKVATQKHROSPLNWTSSHFGE 66
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XX Qy 61 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRNGGTCVLGSCFVCPAHTGRYCEHQR 120
XX Db 67 VTGSAEGWGPEEPLPYSRAFEGEGASAPRCRNGGTCVLGSCFVCPAHTGRYCEHQR 126
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XX Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSL 186
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XX Qy 181 LLPCALLHRLLRDPAPAHPRSLVPSVLQRRRRCGRFGLGHLR 223
XX Db 187 LLPCALLHRLLRDPAPAHPRSLVPSVLQRRRRCGRFGLGHLR 229
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XX RESULT 6
XX ABJ05749
XX ID ABJ05749 standard; protein; 229 AA.
XX AC ABJ05749;
XX XX
XX DT 14-NOV-2002 (first entry)
XX XX

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DE XX Novel human protein SEQ ID No 98.

KW Immunostimulant; antirheumatic; antiarthritic; neuroprotective;

KW antiallergic; antidiabetic; antiasthmatic; antiinflammatory; nootropic;

KW immunosuppressive; anticoagulant; thrombolytic; antiatherosclerotic;

KW cytosstatic; nephroprotective; antiparkinsonian; gynecological; virucide;

KW antibacterial; antiarrhythmic; fungicide; HCPAT05; HMAAE95; HTNBM01;

KW immunodeficiency; autoimmune disorder; allergic reaction; cardiovascular;

KW inflammatory condition; graft-versus-host disease; reproductive system;

KW blood-related disorder; hyperproliferative; endocrine; neurological;

KW respiratory; renal; infectious disease; gastrointestinal; gene therapy;

KW neuronal growth; neuronal disorder; neuro-degenerative condition;

KW keratinocyte growth; human.

OS Homo sapiens.

XX US2002086330-A1.

XX 04-JUL-2002.

XX 17-JAN-2001; 2001US-00764893.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 28-JUN-2000; 2000US-0214886P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 14-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220983P.

XX 26-JUL-2000; 2000US-0220984P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225267P.

XX 14-AUG-2000; 2000US-0225268P.

XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

XX 14-AUG-2000; 2000US-0225758P.

XX 22-AUG-2000; 2000US-0226868P.

XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0229287P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 01-SEP-2000; 2000US-0229345P.

XX 05-SEP-2000; 2000US-0229509P.

XX 05-SEP-2000; 2000US-0229513P.

XX 08-SEP-2000; 2000US-0231143P.

XX 21-SEP-2000; 2000US-0234223P.

XX 21-SEP-2000; 2000US-0234274P.

XX 25-SEP-2000; 2000US-0234997P.

XX 27-SEP-2000; 2000US-0235834P.

XX 29-SEP-2000; 2000US-0236327P.

XX 29-SEP-2000; 2000US-0236367P.

XX 29-SEP-2000; 2000US-0236368P.

XX 29-SEP-2000; 2000US-0236369P.

XX 29-SEP-2000; 2000US-0236370P.

XX 02-OCT-2000; 2000US-0236802P.

XX 02-OCT-2000; 2000US-0237037P.

XX 02-OCT-2000; 2000US-0237038P.

XX 02-OCT-2000; 2000US-0237039P.

XX 02-OCT-2000; 2000US-0237040P.

XX 13-OCT-2000; 2000US-0239935P.

XX 20-OCT-2000; 2000US-0240960P.

XX 20-OCT-2000; 2000US-0241785P.

XX 01-NOV-2000; 2000US-0244617P.

XX 17-NOV-2000; 2000US-0249299P.

XX 08-DEC-2000; 2000US-0251856P.

XX 08-DEC-2000; 2000US-0251868P.

XX 08-DEC-2000; 2000US-0251869P.

PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (BARA/) BARASH S C.

XX Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-665432/71.

XX Novel polypeptide useful for diagnosis, prognosis, prevention, and

PT treatment of immune, hyperproliferative, renal, respiratory,

PT cardiovascular, reproductive, endocrine, gastrointestinal and

PT neurological disorders.

XX Disclosure; Page 268-269; 335pp; English.

XX The invention relates to an isolated polypeptide comprising a sequence at

CC least 90% identical to a full length protein sequence selected from 55

CC sequences given in the specification such as a sequence of 163, 74 or 140

CC amino acids fully defined in the specification, or the encoding sequence

CC contained in 49 cDNA clones given in specification e.g. HCPAT05, HMAAE95

CC or HTNBM01. The protein and its encoding nucleic acid are useful for

CC diagnosing a pathological condition or susceptibility to a pathological

CC condition in a subject and for preventing, treating or ameliorating a

CC medical condition. The protein, its encoding nucleic acid and an isolated

CC antibody that can bind to the protein are useful in treating, preventing,

CC diagnosing and/or prognosing immunodeficiencies, autoimmune disorders,

CC allergic reactions and conditions, inflammatory conditions, graft-versus-

CC renal disorders, cardiovascular disorders, hyperproliferative disorders,

CC neurological disorders, endocrine disorders, reproductive disorders,

CC disorders, infectious diseases, and gastrointestinal disorders. The

CC protein of the invention is useful to stimulate neuronal growth and to

CC treat, prevent, and/or diagnose neuronal damage which occurs in certain

CC neuronal disorders or neuro-degenerative conditions, for stimulating

CC keratinocyte growth, to prevent hair loss, to modulate mammalian

CC characteristics such as body height, weight, hair color, and to increase

CC or decrease storage capabilities, fat content, lipid, protein,

CC carbohydrate, vitamins, minerals, cofactors or other nutritional

CC components. The nucleic acid of the invention can be used in gene

CC therapy. This sequence represents a novel human protein of the invention

XX

SQ Sequence 229 AA;

Query Match 100.0%; Score 223; DB 5; Length 229;

Best Local Similarity 100.0%; Pred. No. 1.5e-195;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHRSPLNWTSSHFG 60

DB 7 MTWRHHVRLFTVSLALQIINLGNYSQREKHNGRGVTKVATQKHRSPLNWTSSHFG 66

QY 61 VTGSAGWGPEPLPYSRAPFGASARPCCRNGGTCVLGSCFVCPAFTGRCYCEHDQRR 120

DB 67 VTGSAGWGPEPLPYSRAPFGASARPCCRNGGTCVLGSCFVCPAFTGRCYCEHDQRR 126

QY 121 SECGALEHGAWTIRACHLCRCIFGALHCLPLOTDPDCDKDFLASHAHGSGAGPSLLL 180

DB 127 SECGALEHGAWTIRACHLCRCIFGALHCLPLOTDPDCDKDFLASHAHGSGAGPSLLL 186

QY 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHL 223

DB 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGGLGHL 229

RESULT 7

ABP66887

ID ABP66887 standard; protein; 229 AA.

XX

AC ABP66887;

XX

DT 09-DEC-2002 (first entry)

XX

DE Human polypeptide SEQ ID NO 608.

XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antispasmodic; antianemic; antiarthritic; cancer;
KW antirheumatic; hepatotrophic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW anticardiac; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX US2002090672-A1.
XX
XX 11-JUL-2002.
XX
XX 17-JAN-2001; 2001US-00764853.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217456P.
PR 14-JUL-2000; 2000US-0218280P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 22-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226668P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 03-SEP-2000; 2000US-0229345P.
PR 03-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 23-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236389P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251869P.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;

XX WPI; 2002-681727/73.
DR N-PSDB; ABV83859.
XX
XX Novel polypeptide useful for diagnosis, prognosis, prevention, and
PT treatment of immune, hyperproliferative, renal, respiratory,
PT cardiovascular, reproductive, endocrine, gastrointestinal and
PT neurological disorders.
XX
XX Claim 11; SEQ ID NO 608; 369pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABV83682-ABV84101) and proteins
CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 229 AA;
XX
Query Match 100.0%; Score 223; DB 5; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-195;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTRHVRLLFTVSLALQIIINLGNYSQREKHNGRGEVTKVATQKHQSPINWTSHPGE 60
Db 7 MTRHVRLLFTVSLALQIIINLGNYSQREKHNGRGEVTKVATQKHQSPINWTSHPGE 66
Qy 61 VTGSAGWGPEEPLPYSRAGEGASAPRCRCRNGGTCVLGSCVCPAHFTGRYCEHQR 120
Db 67 VTGSAGWGPEEPLPYSRAGEGASAPRCRCRNGGTCVLGSCVCPAHFTGRYCEHQR 126
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAGPSAGAPSL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRRRCGRPGLGHL 229
RESULT 8
AB890336
ID AB890336 standard; protein; 223 AA.
XX
AC AB890336;
XX
DT 24-MAY-2002 (first entry)
XX
XX Human polypeptide SEQ ID NO 2712.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotrophic; antidiabetic; antiinflammatory; antitumor;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
XX WO200190304-A2.
XX
XX 29-NOV-2001.

XX PF 18-MAY-2001; 2001WO-US016450.
 XX PR 19-MAY-2000; 2000US-0205515P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;
 XX WPI; 2002-122018/16.
 DR N-PSDB; ABL90745.
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX PS Claim 11; SEQ ID NO 2712; 2081pp + Sequence Listing; English.
 XX CC The invention relates to novel genes (ABL9449-ABL90853) and proteins
 CC (ABB9040-ABB9044) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 223 AA;
 Query Match 83.9%; Score 187; DB 5; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.3e-162;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPLPYSRAFGEGASARPCCRNGGT 96
 DB 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPLPYSRAFGEGASARPCCRNGGT 96
 QY 97 CVLGSCVCPAHTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTDDR 156
 DB 97 CVLGSCVCPAHTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTDDR 156
 QY 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVQLQRRPCGR 216
 DB 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVQLQRRPCGR 216
 QY 217 PGLGHRLL 223
 DB 217 PGLGHRLL 223
 RESULT 9
 ABUS6711
 ID ABUS6711 standard; protein; 223 AA.
 XX AC ABUS6711;
 XX DT 02-APR-2003 (first entry)
 XX DE Lung cancer-associated polypeptide #304.
 XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS WO200286443-A2.
 PN 31-OCT-2002.
 XX 18-APR-2002; 2002WO-US012476.
 PF 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Aziz N, Murray R;
 PI WPI; 2003-093161/08.
 DR N-PSDB; ABX76440.
 DR Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX Claim 27; Page 426; 453pp; English.
 PS The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX Sequence 223 AA;
 Query Match 83.9%; Score 187; DB 6; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.3e-162;
 Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPLPYSRAFGEGASARPCCRNGGT 96
 DB 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPLPYSRAFGEGASARPCCRNGGT 96
 QY 97 CVLGSCVCPAHTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTDDR 156
 DB 97 CVLGSCVCPAHTGTRYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLOTDDR 156
 QY 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVQLQRRPCGR 216
 DB 157 CDPKDFLASHAGPSAGGAPSLLLLLPCALLHRLRPDAPAHPRSLVPSVQLQRRPCGR 216
 QY 217 PGLGHRLL 223
 DB 217 PGLGHRLL 223

```

RESULT 10
ADN39104
ID  ADN39104 standard; protein; 223 AA.
XX
AC  ADN39104;
XX
DT  17-JUN-2004 (first entry)
XX
DE  Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:422.
XX
KW  Human; differential expression; cancer; angiogenic disorder;
KW  fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW  inflammatory disease; autoimmune disease;
KW  retinal neovascularisation syndrome; scarring; uterine fibroid;
KW  detection; diagnosis; prognosis; drug screening; drug targeting;
KW  wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW  vulneryary; gene therapy; vaccine.
XX
OS  Homo sapiens.
XX
XX  WO2003042661-A2.
XX
XX  22-MAY-2003.
XX
XX  13-NOV-2002; 2002WO-US036810.
XX
XX  13-NOV-2001; 2001US-0350666P.
XX  21-NOV-2001; 2001US-0332464P.
XX  29-NOV-2001; 2001US-0334393P.
XX  03-DEC-2001; 2001US-0335394P.
XX  14-DEC-2001; 2001US-0340376P.
XX  08-JAN-2002; 2002US-0347211P.
XX  10-JAN-2002; 2002US-0347349P.
XX  08-FEB-2002; 2002US-035250P.
XX  13-FEB-2002; 2002US-0356714P.
XX  20-FEB-2002; 2002US-0359077P.
XX  29-MAR-2002; 2002US-036809P.
XX  04-APR-2002; 2002US-0370110P.
XX  12-APR-2002; 2002US-0372246P.
XX  05-JUN-2002; 2002US-0386614P.
XX  16-JUL-2002; 2002US-0396839P.
XX  22-JUL-2002; 2002US-0397775P.
XX  22-JUL-2002; 2002US-0397845P.
XX  09-SEP-2002; 2002US-0409450P.
XX
PA  (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX  Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX  Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX  WPI; 2003-468649/44.
XX  N-PSDB; ADN39103.
XX
PT  Determining the presence or absence of a pathological cell in a patient,
PT  useful for diagnosing, prognosing or treating cancer, comprises detecting
PT  a nucleic acid in a biological sample.
XX
XX  Claim 12; SEQ ID NO 422; 1385pp; English.
XX
XX  The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX  whose expression is upregulated or downregulated in specific cancers or
XX  other diseases such as angiogenic or fibrotic disorders, and to methods
XX  of determining the presence or absence of a pathological cell in a
XX  patient by detecting a nucleic acid at least 80% identical to those of
XX  the invention or by detecting a polypeptide of the invention. The
XX  invention also relates to expression vectors and host cells comprising a
XX  nucleic acid of the invention; antibodies which specifically bind a
XX  polypeptide of the invention; use of such antibodies for drug targeting;
XX  and methods of screening for modulators of activity or expression of the
XX  polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX  antibodies and methods are useful for diagnosing, prognosing and treating

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cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularisation syndrome, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ  Sequence 223 AA;
    Query Match      83.9%; Score 187; DB 7; Length 223;
    Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;
    Matches 187; Conservative 0; Mismatches 0;
Qy  37 EVTKVATQKRRQSPLNWTSSTSHFGVETGSAEGWGPEEPLPYSAFGEASARPCRCNGGT 96
Dy  37 EVTKVATQKRRQSPLNWTSSTSHFGVETGSAEGWGPEEPLPYSAFGEASARPCRCNGGT 96
Qy  97 CVLGSPVCVPAHFTGRVCEHQRSECGALHGAHTLRAACHLCRCIFGALHCLPLQTPDR 156
Dy  97 CVLGSPVCVPAHFTGRVCEHQRSECGALHGAHTLRAACHLCRCIFGALHCLPLQTPDR 156
Qy  157 CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLRLPDAPAHPRSLVPSVLQRRRRPCGR 216
Dy  157 CDPKDFLASHAHGPSAGGAPSLLLLLPCALLHRLRLPDAPAHPRSLVPSVLQRRRRPCGR 216
Qy  217 PGLGHRL 223
Dy  217 PGLGHRL 223
RESULT 11
ADN39975
ID  ADN39975 standard; protein; 223 AA.
XX
AC  ADN39975;
XX
DT  17-JUN-2004 (first entry)
XX
DE  Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C345.
XX
KW  Human; differential expression; cancer; angiogenic disorder;
KW  fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW  inflammatory disease; autoimmune disease;
KW  retinal neovascularisation syndrome; scarring; uterine fibroid;
KW  detection; diagnosis; prognosis; drug screening; drug targeting;
KW  wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW  vulneryary; gene therapy; vaccine.
XX
OS  Homo sapiens.
XX
XX  WO2003042661-A2.
XX
XX  22-MAY-2003.
XX
XX  13-NOV-2002; 2002WO-US036810.
XX
XX  13-NOV-2001; 2001US-0350666P.
XX  21-NOV-2001; 2001US-0332464P.
XX  29-NOV-2001; 2001US-0334393P.
XX  03-DEC-2001; 2001US-0335394P.
XX  14-DEC-2001; 2001US-0340376P.
XX  08-JAN-2002; 2002US-0347211P.
XX  10-JAN-2002; 2002US-0347349P.
XX  08-FEB-2002; 2002US-035250P.
XX  13-FEB-2002; 2002US-0356714P.
XX  20-FEB-2002; 2002US-0359077P.
XX  29-MAR-2002; 2002US-036809P.
XX  04-APR-2002; 2002US-0370110P.
XX  12-APR-2002; 2002US-0372246P.
XX  05-JUN-2002; 2002US-0386614P.
XX  16-JUL-2002; 2002US-0396839P.
XX  22-JUL-2002; 2002US-0397775P.
XX  22-JUL-2002; 2002US-0397845P.
XX  09-SEP-2002; 2002US-0409450P.
XX
PA  (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX  Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX  Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX  WPI; 2003-468649/44.
XX  N-PSDB; ADN39103.
XX
PT  Determining the presence or absence of a pathological cell in a patient,
PT  useful for diagnosing, prognosing or treating cancer, comprises detecting
PT  a nucleic acid in a biological sample.
XX
XX  Claim 12; SEQ ID NO 422; 1385pp; English.
XX
XX  The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX  whose expression is upregulated or downregulated in specific cancers or
XX  other diseases such as angiogenic or fibrotic disorders, and to methods
XX  of determining the presence or absence of a pathological cell in a
XX  patient by detecting a nucleic acid at least 80% identical to those of
XX  the invention or by detecting a polypeptide of the invention. The
XX  invention also relates to expression vectors and host cells comprising a
XX  nucleic acid of the invention; antibodies which specifically bind a
XX  polypeptide of the invention; use of such antibodies for drug targeting;
XX  and methods of screening for modulators of activity or expression of the
XX  polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX  antibodies and methods are useful for diagnosing, prognosing and treating

```

XX PA	(EOSB-) EOS BIOTECHNOLOGY INC.	PD 31-MAR-2005.
XX PI	Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevezi PA;	XX 14-SEP-2004; 2004WO-US029967.
XX PI	Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;	XX 15-SEP-2003; 2003US-0503046P.
XX DR	WPI; 2003-458649/44.	XX (RERE-) RES DEV FOUND.
XX DR	N-PSDB; ADN39758.	XX Vale W, Gray PC, Harrison CA;
XX PT	Determining the presence or absence of a pathological cell in a patient,	XX WPI; 2005-242562/25.
XX PT	useful for diagnosing, prognosing or treating cancer, comprises detecting	XX Augmenting signaling of a ligand of receptor serine kinase in a cell
XX PT	a nucleic acid in a biological sample.	XX comprises inhibiting the formation of complexes between Cripto and the
XX PS	Claim 12; SEQ ID NO C345; 1385pp; English.	XX ligand on the surface of the cell.
XX CC	The invention relates to nucleic acids and proteins (ADN38683-ADN40064)	XX Disclosure; SEQ ID NO 4; 60pp; English.
XX CC	whose expression is upregulated or downregulated in specific cancers or	XX This invention relates to a novel method for augmenting signaling of a
XX CC	other diseases such as angiogenic or fibrotic disorders, and to methods	XX ligand of a receptor serine kinase within a cell by inhibiting the
XX CC	of determining the presence or absence of a pathological cell in a	XX formation of complexes between Cripto and this ligand on the surface of
XX CC	patient by detecting a nucleic acid at least 80% identical to those of	XX the cell. Specifically, it refers to TGF-beta and activin which are the
XX CC	the invention or by detecting a polypeptide of the invention. The	XX ligands of serine kinase receptors and which regulate tissue homeostasis
XX CC	invention also relates to expression vectors and host cells comprising a	XX by activating the Smad2/3 intracellular signaling pathway; disruption of
XX CC	nucleic acid of the invention; antibodies which specifically bind a	XX this signaling pathway is associated with oncogenesis and tumorigenesis.
XX CC	polypeptide of the invention; use of such antibodies for drug targeting;	XX As such, the present invention describes a method for augmenting Smad2/3
XX CC	and methods of screening for modulators of activity or expression of the	XX signaling in a cell by administering a mutant ligand that retains
XX CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,	XX signaling activity but is unable to bind to Cripto, and thus bypasses
XX CC	antibodies and methods are useful for diagnosing, prognosing and treating	XX antagonism by Cripto. Note that augmentation of signaling increases
XX CC	cancer and other conditions such as psoriasis, ischaemia, heart disease,	XX phosphorylation and activation of Smad2 and Smad3 in the cell, such that
XX CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal	XX it decreases the proliferative rate of the cell. The receptor serine
XX CC	neovascularization syndromes, scarring and uterine fibroids. They may	XX kinase is a type I activin receptor-like kinases-4 or -5 (ALK-4 or ALK-5)
XX CC	also be useful in wound healing and in contraception. The present	XX and the formation of complexes is inhibited by suppressing expression of
XX CC	sequence represents a polypeptide of the invention.	XX Cripto using antisense oligonucleotides (siRNA) directed against Cripto,
XX SQ	Sequence 223 AA;	XX and also mutating at least one allele of Cripto by homologous
	Query Match 83.9%; Score 187; DB 7; Length 223;	XX recombination. Accordingly, pharmaceutical compositions derived thereof
	Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;	XX exhibit cytostatic activity. This polypeptide sequence is the human
	Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX Criptic protein, a member of the EGF-CFC (Epidermal Growth Factor-Cripto,
		XX FRL-1, Criptic) family of proteins of the invention.
Qy 37	EVTKVATQKHRQSPNLTSSHFGEVGTGSAGWGMPPEPLPYSRAFGEGASARPCCRNGGT 96	XX Sequence 223 AA;
Db 37	EVTKVATQKHRQSPNLTSSHFGEVGTGSAGWGMPPEPLPYSRAFGEGASARPCCRNGGT 96	Query Match 83.9%; Score 187; DB 9; Length 223;
Qy 97	CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156	Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;
Db 97	CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156	Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 157	CDPKDFLASHANGPSAGGAPSLLLLPALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216	Qy 37 EVTKVATQKHRQSPNLTSSHFGEVGTGSAGWGMPPEPLPYSRAFGEGASARPCCRNGGT 96
Db 157	CDPKDFLASHANGPSAGGAPSLLLLPALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216	Db 37 EVTKVATQKHRQSPNLTSSHFGEVGTGSAGWGMPPEPLPYSRAFGEGASARPCCRNGGT 96
Qy 217	PGLGHRLL 223	Qy 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 217	PGLGHRLL 223	Db 97 CVLGSCFCVCPAHTGTRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
RESULT 12		Qy 157 CDPKDFLASHANGPSAGGAPSLLLLPALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216
ID ADY85963	ADY85963 standard; protein; 223 AA.	Db 157 CDPKDFLASHANGPSAGGAPSLLLLPALLHLLRPDAPAHPRSLVPSVLQRRPCGR 216
XX AC	ADY85963;	Qy 217 PGLGHRLL 223
XX XX		Db 217 PGLGHRLL 223
XX DT	16-JUN-2005 (first entry)	RESULT 13
XX DE	Human Criptic protein, a member of the EGF-CFC family Seq 4.	AAU16957
XX XX		ID AAU16957 standard; protein; 231 AA.
XX KW	cell signaling; oncogenesis; antisense therapy; cytostatic; mutagenesis;	XX AAU16957;
XX KW	protein interaction; oncoprotein.	XX AAU16957;
XX OS	Homo sapiens.	XX 07-NOV-2001 (first entry)
XX PN	W02005028433-A2.	XX Human novel secreted protein, SEQ ID 198.
XX XX		XX

KW Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW cardiac; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
OS Homo sapiens.
XX
XX WO200155441-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US0011320.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
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PR 05-SEP-2000; 2000US-0229513P.
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PR 06-SEP-2000; 2000US-0230438P.
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PR 08-SEP-2000; 2000US-0232080P.
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PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 08-NOV-2000; 2000US-0246478P.
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PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
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PR 17-NOV-2000; 2000US-0249297P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
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PR 05-DEC-2000; 2000US-0256719P.

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PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254037P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476222/51.
XX N-PSDB; AAS26862.
XX
XX Novel polypeptides and polynucleotides useful as diagnostic reagents to
XX diagnose diseases or disorders associated with aberrant expression or
XX activity of polypeptides, for treating blood clotting disorder,
XX hemophilia.
XX
XX Claim 11; SEQ ID NO 198; 601pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
XX encoded secreted proteins. The nucleic acids and proteins are used to
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
XX in diagnosing a pathological condition or susceptibility to a
XX pathological condition. Antibodies to the proteins can also be used in
XX alleviating symptoms associated with the disorders and in diagnostic
XX immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
XX (ELISA). Disorders which are diagnosed or treated include autoimmune
XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
XX neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
XX arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
XX nervous system disorders e.g. Alzheimer's disease, infections caused by
XX bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
XX and many other disorders listed in the specification. The polypeptides
XX can also be used to aid wound healing and epithelial cell proliferation,
XX to prevent skin aging due to sunburn, to maintain organs before
XX transplantation, for supporting cell culture of primary tissues, to
XX regenerate tissues and in chemotaxis. The polypeptides can also be used
XX as a food additive or preservative to increase or decrease storage
XX capabilities, fat content, lipid, protein, carbohydrate, vitamins,
XX minerals, cofactors and other nutritional components. The present
XX sequence represents a novel secreted protein of the invention. Note: The
XX
XX Query Match 83.9%; Score 187; DB 4; Length 231;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-162; Indels 0; Gaps 0;
XX Matches 187; Conservative 0; Mismatches 0;
XX
XX QY 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96
XX Db 45 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 104
XX
XX QY 97 CVLGSCFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
XX Db 105 CVLGSCFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164
XX
XX QY 157 CDPKDFLASHAHGSPSAGGAPSLLLLPALLHLLRPDAPAHPSLVPSVLQRRPCGR 216
XX Db 165 CDPKDFLASHAHGSPSAGGAPSLLLLPALLHLLRPDAPAHPSLVPSVLQRRPCGR 224
XX
XX QY 217 PGLGHRL 223
XX Db 225 PGLGHRL 231
XX
XX RESULT 14
XX AAW09111
XX ID AAW09111 standard; protein; 230 AA.
XX
XX AC AAW09111;
```

```
XX 16-APR-1997 (first entry)
XX DT
XX DE Human criptin growth factor.
XX
XX KW Criptin growth factor; CGF; angiogenesis; wound healing; vulnery;
XX KW muscle wastage; osteoporosis; implant fixation; tissue regeneration;
XX KW pancreas cancer; diagnosis; gene therapy.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT /label= Sig_peptide
XX
XX PN WO9639420-A1.
XX
XX PD 12-DEC-1996.
XX
XX PF 05-JUN-1995; 95WO-US007087.
XX
XX PR 05-JUN-1995; 95WO-US007087.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA Meissner PS, Coleman TA;
XX
XX PI WPI; 1997-043055/04.
XX
XX DR N-PSDB; AAT51058.
XX
XX New isolated human Criptin Growth Factor polypeptide - which can be used
XX to stimulate angiogenesis and develop products for use in diagnosis and
XX therapy.
XX
XX Claim 12; Fig 1; 52pp; English.
XX
XX Human criptin growth factor (CGF) (AAW09111) is a novel polypeptide
XX structurally related to human cripto growth factor. It is overexpressed
XX and secreted by certain types of cancer cells, e.g. pancreatic cancers.
XX Recombinant CGF can be produced in host cells utilising vectors
XX incorporating a CGF cDNA clone (AAT51058) isolated from a human
XX pancreatic cancer tissue cDNA library. CGF can be used to treat e.g.
XX muscle wasting diseases, osteoporosis, to aid implant fixation, to
XX stimulate tissue regeneration and wound healing, to promote angiogenesis
XX and to stimulate proliferation of vascular smooth muscle and endothelial
XX cell prodn. It can also be used as a marker for cancer diagnosis
XX
XX SQ Sequence 230 AA;
XX
XX Query Match 66.8%; Score 149; DB 2; Length 230;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-128; Indels 0; Gaps 0;
XX Matches 149; Conservative 0; Mismatches 0;
XX
XX QY 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96
XX Db 37 EVTKVATQKHRSPLNWTSSHFGEVTSAGWGPEEPPLYSRAFGEGASARPCCRNGGT 96
XX
XX QY 97 CVLGSCFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
XX Db 97 CVLGSCFCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
XX
XX QY 157 CDPKDFLASHAHGSPSAGGAPSLLLLPALLPCA 185
XX Db 157 CDPKDFLASHAHGSPSAGGAPSLLLLPALLPCA 185
XX
XX RESULT 15
XX AAG77914
XX ID AAG77914 standard; protein; 223 AA.
XX
XX AC AAG77914;
XX
XX DT 23-JAN-2002 (first entry)
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:52:05 ; Search time 297 Seconds
(without alignments)
694.540 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRVHVRLLFTSLALQII.....PSVLQRERRPCRGPLGHLRL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 6

Total number of hits satisfying chosen parameters: 11635

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	187	83.9	223	1	CFC1_HUMAN
2	15.	6.7	202	1	P97766 mus musculus
3	14	6.3	191	2	Q2UZ56 XENLA
4	14	6.3	191	2	Q2VU96 XENLA
5	11	4.9	179	2	Q2VU94 XENLA
6	11	4.9	251	2	Q2UZ94 XENLA
7	11	4.9	251	2	Q2VU93 XENLA
8	8	3.6	105	2	Q53M57 ORYSA
9	8	3.6	105	2	Q60E85 ORYSA
10	8	3.6	158	2	Q5R263 DROSE
11	8	3.6	158	2	Q5R293 DROSI
12	8	3.6	158	2	Q9V901 DROME
13	8	3.6	346	2	Q5WB00 BACSK
14	8	3.6	353	2	Q5F349 CHICK
15	8	3.6	357	2	Q3P026 SGMM
16	8	3.6	375	2	Q4RMCI TETNG
17	8	3.6	382	2	Q7QV27 GIALA
18	8	3.6	384	2	Q37YV8 SPHAR
19	8	3.6	409	2	Q43ZW8 SOLUS
20	8	3.6	415	2	Q4B045 BURK
21	8	3.6	456	1	GUNA_MICBI
22	8	3.6	655	2	Q8ST54 ENCCU
23	8	3.6	701	2	Q41C80 9BACI
24	8	3.6	721	2	Q7XQ88 ORYSA
25	8	3.6	752	2	Q42374 BRARE
26	8	3.6	762	2	Q4RS94 brachydanio
27	8	3.6	793	2	Q13876 HUMAN
28	8	3.6	823	2	Q6X220 bovine herp
29	8	3.6	859	1	OBP_BHVIC
30	8	3.6	924	2	Q4DT24 TRYCR
31	8	3.6	927	2	Q4E329 trypanosoma

32	8	3.6	1046	2	Q4S1V9 TETNG
33	8	3.6	1085	2	Q3FR67 rhodofexax
34	8	3.6	1152	2	Q4J8A9 SULAC
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36	8	3.6	1230	2	Q4G0F4 HUMAN
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39	8	3.6	2030	2	Q4RHP2 TETNG
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43	8	3.6	2819	2	Q6W4W6 CHICK
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Q4S1V9	tetraodon n
Q3FR67	rhodofexax
Q4J8A9	sulfolobus
O0411	homo sapien
Q4G0F4	homo sapien
Q4RJ05	tetraodon n
Q4RQ96	tetraodon n
Q4RHP2	tetraodon n
Q4SRM9	tetraodon n
Q800E4	brachydanio
P21783	xenopus lae
Q6W4W6	gallus gall
Q4RXP0	tetraodon n
Q6LDJ0	homo sapien

ALIGNMENTS

RESULT 1
CFC1_HUMAN
ID_CFC1_HUMAN STANDARD; PRT; 223 AA.
AC Q9GZJ3; Q53T05;
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Cryptic protein precursor.
GN Name=CFC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP CYS-112, CHARACTERIZATION OF VARIANT HTX2 CYS-112, AND VARIANTS TRP-78 AND CYS-189.
RX MEDLINE=20517351; PubMed=1062482; DOI=10.1038/81695;
RA Bamford R.N., Roesler E., Burdine R.D., Saplakoglu U., dela Cruz J., Splitt M., Towbin J., Bowers P., Marino B., Schier A.F., Shen M.M., Muenke M., Casey B.;
RA "Loss-of-function mutations in the EGF-CFC gene CFC1 are associated with human left-right laterality defects";
Nat. Genet. 26:365-369(2000).
RL [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA], AND VARIANT TRP-78.
RP PubMed=15815621; DOI=10.1038/nature03466;
RX Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H., Minx P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M., Becker M.C., Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Krentzki C., Oddi L., Du H., Sun H., Bradshaw-Cordum H., Ali J., Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C., Du F., Courtney L., Kalicki J., Ozersky P., Abbott S., Armstrong J., Belter E.A., Caruso L., Cedroni M., Cotton M., Davidson T., Desai A., Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K., Holmes A., Hartings R., Kim K., Kruchowski S.S., Strong C.M., Grewal N., Goyea E., Hou S., Levy A., Martinka S., Mead K., McEllean M.B., Meyer R., Randall-Maher J., Tomlinson C., Dauphin-Kohlberg S., Kozlowski-Reilly A., Shah N., Sweatengen-Shahid S., Snider J., Strong J.T., Thompson J., Yoakum M., Leonard S., Pearson C., Trani L., Radionenko M., Waligorski J.E., Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P., Wendl M.C., Yang S.-P., Pohl C., Wallis J.W., Spieth J., Bieri T.A., Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A., Shatland Y., Sinha P., Wohlmann P.E., Cook L.L., Hickenbotham M.T., Eldred J., Williams D., Jones T.A., She X., Ciccarelli F.D., Izaurralde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X., McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C., Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Furey T.S., Miller W., Eichler E.E., Bork P., Suyama M., Torrents D., Waterston R.H., Wilson R.K.;
RT "Generation and annotation of the DNA sequences of human chromosomes 2 and 4.";

```

RL Nature 434:724-731(2005).
RN [3]
RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RX PubMed=11799476;
RA Goldmuntz E., Bamford R., Karkera J.D., dela Cruz J., Roessler E.,
RA Muenke M.;
RT "CFCL mutations in patients with transposition of the great arteries
RT and double-outlet right ventricle.";
RL Am. J. Hum. Genet. 70:776-780(2002).
CC -I- FUNCTION: Involved in the correct establishment of the left-right
CC axis. May play a role in mesoderm and/or neural patterning during
CC gastrulation.
CC -I- PTM: N-glycosylated [By similarity].
CC -I- DISEASE: Defects in CFCL are a cause of visceral heterotaxy (HTX2)
CC [MIM:605376]. HTX2 is an autosomal form of visceral heterotaxy
CC (HTX). HTX is characterized by a variable group of congenital
CC anomalies that include complex cardiac malformations and situs
CC inversus or situs ambiguus.
CC -I- DISEASE: Defects in CFCL are a cause of transposition of the great
CC arteries, dextro-looped (DTGA) [MIM:608808]. The more common form
CC of DTGA, consists of complete inversion of the great vessels, so
CC that the aorta incorrectly arises from the right ventricle and the
CC pulmonary artery incorrectly arises from the left ventricle. This
CC creates completely separate pulmonary and systemic circulatory
CC systems, an arrangement that is incompatible with life. Patients
CC often have atrial and/or ventricular septal defects or other types
CC of shunting that allow some mixing between the circulations in
CC order to support life minimally, but surgical intervention is
CC always required.
CC -I- DISEASE: Defects in CFCL are a cause of conotruncal heart
CC malformations (CTHM) [MIM:217095]. CTHM consist of cardiac outflow
CC tract defects, such as tetralogy of Fallot, pulmonary atresia,
CC double-outlet right ventricle, truncus arteriosus communis, and
CC aortic arch anomalies.
CC -I- SIMILARITY: Contains 1 EGF-like domain.
CC -----
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CC -----
DR ENBL; AF312769; AAG30294.1; -; mRNA.
DR ENBL; AF312925; AAG42475.1; -; Genomic DNA.
DR ENBL; AC013269; AAY14955.1; -; Genomic_DNA.
DR ENBL; BC069508; AHH69508.1; -; mRNA.
DR ENBL; BC074825; AAH74825.1; -; mRNA.
DR ENBL; BC074826; AAH74826.1; -; mRNA.
DR ENBL; BC110080; AAI10081.1; -; mRNA.
DR HSSP; P00750; 1TPG.
DR HGNC; HGNC:18292; CFCL.
DR MIM; 217095; phenotype.
DR MIM; 605194; gene.
DR MIM; 605376; phenotype.
DR MIM; 608808; P:determination of left/right symmetry; NAS.
DR GO; GO:0007368; P:determination of left/right symmetry; NAS.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR0006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00026; EGF_3; 1.
KW Developmental protein; Disease mutation; EGF-like domain;
KW Gastrulation; Glycoprotein; Polymorphism; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 223 Cryptic protein.
FT DOMAIN 86 115 EGF-like.
FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
FT DISULFID 90 97 By similarity.
FT DISULFID 91 103 By similarity.
FT DISULFID 105 114 By similarity.
FT VARIANT 78 78 R -> W (in dbSNP:2579433).
FT VARIANT 112 112 R -> C (in HTX2; complete loss of
FT activity; abnormal cell surface
FT localization).
FT VARIANT 189 189 R -> C.
FT SEQUENCE 223 AA; 24612 MW; B52852A0ABCFLA3 CRC64;
Query Match 83.9%; Score 187; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.2e-172;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 EVTKVATQKHROSPLNWTSSHFGEVTSAGWGPEEPPLVSRAFGSGASAPRCRCNGGT 96
DB 37 EVTKVATQKHROSPLNWTSSHFGEVTSAGWGPEEPPLVSRAFGSGASAPRCRCNGGT 96
QY 97 CVLGSCFCVCPAIFTGRYCSHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
DB 97 CVLGSCFCVCPAIFTGRYCSHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
QY 157 CDPKDFLASHANGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
DB 157 CDPKDFLASHANGPSAGGAPSLLLLPALLHRLRPDAPAHPRSLVPSVLQRRPCGR 216
QY 217 PGLGHRLL 223
DB 217 PGLGHRLL 223
RESULT 2
CFCL MOUSE STANDARD; PRT; 202 AA.
ID CFCL MOUSE STANDARD; PRT; 202 AA.
AC P97766; Q496U5; Q9JIB7;
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1997, sequence version 1.
DT 07-MAR-2006, entry version 30.
DE Cryptic protein precursor.
GN Name=Cfcl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, TISSUE SPECIFICITY,
RP DEVELOPMENTAL STAGE, AND GLYCOSYLATION.
RC STRAIN=129/SV;
RX MEDLINE=97178978; PubMed=9053319;
RA Shen M.M., Wang H., Leder P.;
RT "A differential display strategy identifies Cryptic, a novel EGF-

```

related gene expressed in the axial and lateral mesoderm during mouse gastrulation."

RL Development 124:429-442(1997).

[2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. DOI=10.1073/pnas.2426038999;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carncini P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-154.
RX MEDLINE=20480687; PubMed=11024280; DOI=10.1016/S0378-1119(00)00337-1;
RA Colas J.-F., Schoenwolf G.C.;
RT "Subtractive hybridization identifies chick-cripto, a novel EGF-CFC
RT ortholog expressed during gastrulation, neurulation and early
RT cardiogenesis."

RL Gene 255:205-217(2000).

[4]

RP FUNCTION, AND KNOCK-OUT.
RX MEDLINE=20045034; PubMed=10574770; DOI=10.1016/S0960-9822(00)80059-7;
RA Gaio U., Schweickert A., Fischer A., Garratt A.N., Mueller T.,
RA Ozcelik C., Lankes W., Strehle M., Britsch S., Blum M.,
RA Birmehmer C.;
RT "A role of the cryptic gene in the correct establishment of the left-
RT right axis."

RL Curr. Biol. 9:1339-1342(1999).

CC -1- FUNCTION: Involved in the correct establishment of the left-right
CC axis. May play a role in mesoderm and/or neural patterning during
CC gastrulation.

CC -1- TISSUE SPECIFICITY: No expressed in adult tissues.

CC -1- DEVELOPMENTAL STAGE: Expressed during gastrulation (from 6.5 dpc
CC to 11 dpc) in two spatial domains that correspond to the axial and
CC lateral mesoderm. In the first domain expression is progressively
CC localized to the anterior primitive streak, the head process, and
CC the node and notochordal. In the second domain, expression is
CC initially concentrated in the lateral region of the egg cylinder,
CC and is later found circumferentially in the intermediate and
CC lateral plate mesoderm. Furthermore, the expression can also be
CC detected at the early head-fold stage in the midline
CC neuroectoderm, and consequently is an early marker for the
CC prospective floor plate of the neural tube. Expression ceases at
CC the end of gastrulation, and has not been observed in later
CC embryonic stages.

CC -1- PTM: N-glycosylated.

CC -1- MISCELLANEOUS: Mice lacking functional Cfcl1 showed positional
CC defects in internal organs. The lung presents a right pulmonary
CC isomerism. The stomach is located on either the left or the right
CC and the spleen is small and has an abnormal shape. The apex of the
CC heart pointed to the right or left. In addition malpositioning of
CC heart outflow tracts is observed, the aorta is connected to the
CC right ventricle and emerged from the heart in a ventral position
CC and to the right of the pulmonary artery. This one is connected to
CC either the left or the right ventricle.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -----

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CC EMBL; U57720; AAC53042.1; -; mRNA.
CC EMBL; BC100705; AA100706.1; -; mRNA.
CC EMBL; BC100706; AA100707.1; -; mRNA.
CC EMBL; BC100708; AA100709.1; -; mRNA.
CC EMBL; BC100711; AA100712.1; -; mRNA.
CC EMBL; AF242430; AAF76323.1; -; Genomic_DNA.
CC HSP; P00749; IURK.
CC Ensembl; ENSMUSG00000026124; Mus musculus.
CC MGI; MGI:109448; Cccl.
CC GO; GO:0005615; C:extracellular space; TAS.
CC InterPro; IPR000742; EGF_3.
CC InterPro; IPR006209; EGF-like.
CC Pfam; PF00008; EGF_1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS50036; EGF_3; 1.
CC Developmental protein; EGF-like domain; Gastrulation; Glycoprotein;
CC Signal.
CC CHAIN 1 35 Potential.
CC DOMAIN 94 123 Cryptic protein.
CC CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
CC DISULFID 98 105 By similarity.
CC DISULFID 99 111 By similarity.
CC DISULFID 113 122 By similarity.
CC CONFLICT 83 83 P -> T (in Ref. 2; AA100707).
CC SEQUENCE 202 AA; 21792 MW; 57035AD339A16FD7 CRC64;
Query Match 6.7%; Score 15; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 NGGTCVLGSGFCVCPA 107
DB 101 NGGTCVLGSGFCVCPA 115

RESULT 3
Q2UZ96 XENLA PRELIMINARY; PRT; 191 AA.
AC Q2UZ96; 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Crpto-2.
GN Name=CR2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT xenopus development."
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; AJ864899; CA115753.1; -; mRNA.
CC SEQUENCE 191 AA; 21651 MW; D4E992122C89495D CRC64;
Query Match 6.3%; Score 14; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 NGGTCVLGSGFCVCP 106

```
Db          93 NGGTCVLGSGFCVCP 106
|||||
RESULT 4
Q2VU96_XENLA PRELIMINARY; PRT; 191 AA.
AC Q2VU96;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE CR2.
GN Names=CR2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
CC -----
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CC -----
DR EMBL; AY796186; AAX81598.1; -; mRNA.
SQ SEQUENCE 191 AA; 21681 MW; 95E9920E40F95531 CRC64;

Query Match      6.3%; Score 14; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 88-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFCVCP 106
|||||
Db          93 NGGTCVLGSGFCVCP 106
|||||
RESULT 5
Q2VU94_XENLA PRELIMINARY; PRT; 179 AA.
AC Q2VU94;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 short transcript variant (Cripto-3 short).
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
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CC -----
DR EMBL; AY796186; AAX81598.1; -; mRNA.
SQ SEQUENCE 191 AA; 21681 MW; 95E9920E40F95531 CRC64;

Query Match      6.3%; Score 14; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 88-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFCVCP 106
|||||
Db          93 NGGTCVLGSGFCVCP 106
|||||
RESULT 6
Q2VU94_XENLA PRELIMINARY; PRT; 251 AA.
AC Q2VU94;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Cripto-3 long.
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Dorey K., Hill C.S.;
RT "Role of EGF-CFC family members in Nodal signalling during early
RT Xenopus development.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ864901; CAI15755.1; -; mRNA.
SQ SEQUENCE 251 AA; 27813 MW; D0256376A829A37E CRC64;

Query Match      4.9%; Score 11; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFC 103
|||||
Db          80 NGGTCVLGSGFC 90
|||||
RESULT 7
Q2VU93_XENLA PRELIMINARY; PRT; 251 AA.
AC Q2VU93;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE CR3 long transcript variant.
GN Names=CR3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16339189; DOI=10.1242/dev.02188;
RA Onuma Y., Yeo C.Y., Whitman M.;
RT "XCR2, one of three Xenopus EGF-CFC genes, has a distinct role in the
RT regulation of left-right patterning.";
RL Development 133:237-250(2006).
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CC -----
DR EMBL; AJ864900; CAI15754.1; -; mRNA.
SQ SEQUENCE 179 AA; 20060 MW; 912E723BE597D6CE CRC64;

Query Match      4.9%; Score 11; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          93 NGGTCVLGSGFC 103
|||||
Db          80 NGGTCVLGSGFC 90
|||||
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CC -----
DR EMBL: AY796189; AAX81599.1; -; mRNA.
KW EGF-like domain, Repeat.
SQ SEQUENCE 251 AA; 27849 MW; DDFCC140A3E0BFE CRC64;

  Query Match      4.9%; Score 11; DB 2; Length 251;
  Best Local Similarity 100.0%; Pred. No. 0.083;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NGGTCVLGSFC 103
Db 152 NGGTCVLGSFC 162

RESULT 8
Q53M57 ORYSA PRELIMINARY; PRT; 105 AA.
AC Q53M57;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Expressed protein.
GN ORFNames=LOC Os11g14190; .
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Tsitrin T.,
RA Bera J., Kim M., Jin S., Fadrosch D., Vuong H., Overton II L.,
RA Reardon M., Weaver B., Johri S., Lewis M., Utterback T., Van Aken S.,
RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Tobst S.,
RA de Vazeilles A., White O., Salzberg S., Fraser C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AC137824; AAX96767.1; -; Genomic DNA.
DR EMBL: DP000010; AB92348.1; -; Genomic DNA.
SQ SEQUENCE 105 AA; 11604 MW; 91390CAC01836B7C CRC64;

  Query Match      3.6%; Score 8; DB 2; Length 105;
  Best Local Similarity 100.0%; Pred. No. 32;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLLP 183
Db 73 PSLLLLLP 80

RESULT 9
Q60E65 ORYSA PRELIMINARY; PRT; 105 AA.
AC Q60E65;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein OSJNBa0073E05.11.
GN Name=OSJNBa0073E05.11;

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OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSJNBa0073E05 genomic sequence.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AC136219; AAV31337.1; -; Genomic DNA.
DR Gramene; Q60E65; .
KW Hypothetical protein.
SQ SEQUENCE 105 AA; 10289 MW; 48FF3E18C287B182 CRC64;

  Query Match      3.6%; Score 8; DB 2; Length 105;
  Best Local Similarity 100.0%; Pred. No. 32;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLLP 183
Db 42 PSLLLLLP 49

RESULT 10
Q5R263 DROSE PRELIMINARY; PRT; 158 AA.
ID Q5R263 DROSE PRELIMINARY; PRT; 158 AA.
AC Q5R263;
DT 04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT 04-JAN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE CG13869.
GN ORFNames=CG13869;
OS Drosophila sechellia (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15729003; DOI=10.1266/ggs.79.351;
RA Kawahara Y., Mateno T., Nozawa M., Shin-I T., Kohara Y., Aigaki T.;
RT "Comparative sequence analysis of a gene-dense region among closely
RT related species of Drosophila melanogaster.";
RL Genes Genet. Syst. 79:351-359 (2004).
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CC -----
DR EMBL: AB162351; BAD72913.1; -; Genomic DNA.
DR FlyBase; FBgn0082773; Dsec/CG13869.
DR InterPro; IPR006631; DUF_DM4_12.
DR Pfam; PF07841; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
SQ SEQUENCE 158 AA; 18628 MW; 752363888A7DDA2B CRC64;

  Query Match      3.6%; Score 8; DB 2; Length 158;
  Best Local Similarity 100.0%; Pred. No. 45;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 LHRLLRP 193
Db 102 LHRLLRP 109

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RESULT 11
QSR293 DROS1 PRELIMINARY; PRT; 158 AA.
AC QSR293;
DT 04-JAN-2005, integrated into UniProtKB/TrEMBL.
DT 04-JAN-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE CG13869.
GN ORFNames=CG13869;
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP PubMed=15729003; DOI=10.1266/ggs.79.351;
RA Kawahara Y., Matsuo T., Nozawa M., Shin-I T., Kohara Y., Aigaki T.;
RT "Comparative sequence analysis of a gene-dense region among closely
RT related species of Drosophila melanogaster.";
RL Genes Genet. Syst. 79:351-359(2004).
CC -----
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CC -----
DR EMBL; AB162349; BAD72895.1; -; Genomic_DNA.
DR FlyBase; FBGN0082752; Dsln\CG13869.
DR InterPro; IPR006631; DUF_DM4_12.
DR Pfam; PF07841; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
SQ SEQUENCE 158 AA; 18589 MW; 4C39B3C6BB06CEB1 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 186 LLHRLRLP 193
Db 102 LLHRLRLP 109

RESULT 12
QSV901 DROME PRELIMINARY; PRT; 158 AA.
AC QSV901;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE CG13869-PA.
GN ORFNames=CG13869, Dmel CG13869;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Brokstein D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtie K.C., Busam D.A., Butler H., Butler E., Center A., Chandra I.,
RA Cherty J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasseer K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stapleton M., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Croiby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
RA FlyBase;
RL Submitted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC -----
DR EMBL; AE003793; AAF57503.1; -; Genomic_DNA.
DR FlyBase; FBgn0034486; CG13869.
DR InterPro; IPR006631; DUF_DM4_12.
DR Pfam; PF07841; DM4_12; 1.
DR SMART; SM00718; DM4_12; 1.
SQ SEQUENCE 158 AA; 18591 MW; 18591 MW; CC28B147B1046DB7 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 LLHRLRP 193
Db 102 LLHRLRP 109

RESULT 13
Q5WB00_BACSK PRELIMINARY; PRT; 346 AA.
AC Q5WB00;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Hypothetical protein.
GN OrderedLocNames=ABC3929;
OS Bacillus clausii (strain KSM-K16).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=66692;
RN [1]
RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA Kawai S., Ito S., Horikoshi K.;
RT "The complete genome sequence of the alkaliphilic Bacillus clausii
RT KSM-K16."
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AP006627; BAD66460.1; -; Genomic_DNA.
DR InterPro; IPR007820; Put_NH3_mOase.
DR Pfam; PF05145; AmoA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 346 AA; 36837 MW; 8BECA0D42874806F CRC64;

Query Match 3.6%; Score 8; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LFTVSLAL 17
Db 51 LFTVSLAL 58

RESULT 14
Q5F349_CHICK PRELIMINARY; PRT; 353 AA.
AC Q5F349;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE Hypothetical protein.
GN ORFNames=RCJMB04_34j1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
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RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis";
RL Genome Biol. 6:R6-R6(2005).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -----
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CC -----
DR EMBL; AJ851801; CAH65435.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Chk_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF07714; Kinase_Tyr; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Receptor; Transferase.
SQ SEQUENCE 353 AA; 40217 MW; 8F045CB5096887F6 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSLLLLL 182
Db 17 APSLLLLL 24

RESULT 15
Q3P0Z6_9GAMM PRELIMINARY; PRT; 357 AA.
AC Q3P0Z6;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Secretion protein HlyD precursor.
GN ORFNames=SdenDRAFT_0315;
OS Shewanella denitrificans OS217.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=318161;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RP US DOE Joint Genome Institute (JGI-PGF);
RC STRAIN=OS-217;
RG Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Shewanella
RT denitrificans OS-217."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OS-217;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Shewanella denitrificans
RT OS-217."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAU001000015; EAM70114.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
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DR GO; GO:0015428; F:type I protein secretor activity; IEA.
 DR GO; GO:0009306; F:protein secretion; IEA.
 DR InterPro; IPR006143; HlyD.
 DR InterPro; IPR003997; RtxD_bac.
 DR PRINTS; PR01490; RTXTOXIND.
 DR TIGRFAMs; TIGR01730; RND_mfp; 1.
 KW Signal.

FT SIGNAL 1 28 Potential.

SQ SEQUENCE 357 AA; 39181 MW; BBB91C4A932116A3 CRC64;

Query Match 3.6%; Score 8; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 LLLPCALL 187

Db 11 LLLPCALL 18

Search completed: September 22, 2006, 19:00:17
 Job time : 302 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:00:34 ; Search time 49 Seconds
(without alignment)
398.354 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRHHVRLFTVSLALQII.....PSVLQRERRPCGRPLGHLRL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1685

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pdp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pdp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pdp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pdp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pdp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pdp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfilese1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	149	66.8	230	1	US-08-471-371-2
2	8	3.6	363	2	US-09-252-991A-18016
3	8	3.6	2523	1	US-08-185-432-18
4	8	3.6	2523	2	US-08-899-232-3
5	8	3.6	2523	2	US-09-121-457-3
6	7	3.1	69	2	US-09-489-039A-9115
7	7	3.1	70	2	US-09-621-976-5356
8	7	3.1	88	2	US-09-621-976-3983
9	7	3.1	103	2	US-09-621-976-5415
10	7	3.1	106	2	US-09-149-476-341
11	7	3.1	107	2	US-09-461-325-484
12	7	3.1	107	2	US-10-012-542-484
13	7	3.1	107	2	US-10-115-123-484
14	7	3.1	111	2	US-09-248-796A-26807
15	7	3.1	112	2	US-09-621-976-3926
16	7	3.1	115	2	US-10-104-047-3840
17	7	3.1	119	2	US-09-991-181-165
18	7	3.1	119	2	US-09-990-444-165
19	7	3.1	119	2	US-09-997-333-165
20	7	3.1	119	2	US-09-922-598-165
21	7	3.1	119	2	US-09-989-735-165
22	7	3.1	119	3	US-09-989-726-165
23	7	3.1	119	3	US-09-997-514-165
24	7	3.1	119	3	US-09-989-728-165
25	7	3.1	119	3	US-09-997-349-165
26	7	3.1	119	3	US-09-997-653-165

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27 7 3.1 119 3 US-09-989-293A-165 Sequence 165, App
28 7 3.1 134 2 US-09-513-999C-4153 Sequence 4153, Ap
29 7 3.1 136 2 US-09-252-991A-32279 Sequence 32279, A
30 7 3.1 155 2 US-09-975-456B-10 Sequence 10, Appl
31 7 3.1 156 2 US-09-615-192A-272 Sequence 272, App
32 7 3.1 165 2 US-08-966-317-1 Sequence 1, Appli
33 7 3.1 165 2 US-09-489-770-1 Sequence 1, Appli
34 7 3.1 172 2 US-09-252-991A-22814 Sequence 22814, A
35 7 3.1 178 2 US-09-252-991A-17622 Sequence 17622, A
36 7 3.1 198 2 US-09-893-737-236 Sequence 236, App
37 7 3.1 204 2 US-09-603-208A-140 Sequence 140, App
38 7 3.1 204 2 US-09-603-208A-142 Sequence 142, App
39 7 3.1 209 2 US-09-893-737-126 Sequence 126, App
40 7 3.1 220 2 US-09-605-703B-1778 Sequence 1778, Ap
41 7 3.1 229 2 US-10-104-047-3041 Sequence 3041, Ap
42 7 3.1 232 2 US-09-248-796A-20904 Sequence 29904, A
43 7 3.1 239 2 US-09-270-767-46338 Sequence 46338, A
44 7 3.1 241 2 US-09-248-796A-21158 Sequence 21158, A
45 7 3.1 259 2 US-09-252-991A-28573 Sequence 28573, A

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ALIGNMENTS

RESULT 1

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US-08-471-371-2
; Sequence 2, Application US/08471371
; Patent No. 5981215
; GENERAL INFORMATION:
; APPLICANT: Meissner, Paul S.
; APPLICANT: Coleman, Timothy A.
; TITLE OF INVENTION: HUMAN CRIPIN GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: N.J.
; COUNTRY: U.S.A
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.371
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 32580-455
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-371-2

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Query Match 66.8%; Score 149; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.7e-136;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 37 EVTKVATQKIQSRQPLNWTSHFGVGTGSAEGWGPEEPYPYSRAFGEASARPCRCRNGGT 96
Db 37 EVTKVATQKIQSRQPLNWTSHFGVGTGSAEGWGPEEPYPYSRAFGEASARPCRCRNGGT 96

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QY 97 CVLGSCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 97 CVLGSCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY 157 CDPKDFLASHAHGPSAGGAPSLLLLPKA 185
Db 157 CDPKDFLASHAHGPSAGGAPSLLLLPKA 185

RESULT 2
US-09-252-991A-18016
; Sequence 18016, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18016
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18016

Query Match 3.6%; Score 8; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 GASARPRC 90
Db 352 GASARPRC 359

RESULT 3
US-08-185-432-18
; Sequence 18, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Buseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matauno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mierock, S. Leslie
; REGISTRATION NUMBER: 19,872
; REFERENCE/DOCKET NUMBER: 7326-006
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-18

Query Match 3.6%; Score 8; DB 1; Length 2523;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CRNGGTCV 98
Db 265 CRNGGTCV 272

RESULT 4
US-08-899-232-3
; Sequence 3, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2523
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-08-899-232-3

Query Match 3.6%; Score 8; DB 2; Length 2523;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CRNGGTCV 98
Db 265 CRNGGTCV 272

RESULT 5
US-09-121-457-3
; Sequence 3, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2523
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-09-121-457-3

Query Match 3.6%; Score 8; DB 2; Length 2523;
Best Local Similarity 100.0%; Pred. No. 85;
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Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      91 CRNGGTCV 98
      |||||
Db      265 CRNGGTCV 272

RESULT 6
US-09-489-039A-9115
; Sequence 9115, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9115
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9115

Query Match      3.1%; Score 7; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 36;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      175 APSLLLL 181
      |||||
Db      8 APSLLLL 14

RESULT 7
US-09-621-976-5356
; Sequence 5356, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5356
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; NAME/KEY: UNSURE
; LOCATION: 39
; OTHER INFORMATION: Xaa = Ala,Pro
US-09-621-976-5356

Query Match      3.1%; Score 7; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 36;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      173 GGAPSL 179
      |||||
Db      60 GGAPSL 66

RESULT 8
US-09-621-976-3983
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; Sequence 3983, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3983
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-3983

Query Match      3.1%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 44;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      175 APSLLLL 181
      |||||
Db      8 APSLLLL 14

RESULT 9
US-09-621-976-5415
; Sequence 5415, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5415
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24...-1
US-09-621-976-5415

Query Match      3.1%; Score 7; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 51;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      175 APSLLLL 181
      |||||
Db      8 APSLLLL 14

RESULT 10
US-09-149-476-341
; Sequence 341, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
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[illegible]

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-08-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 3.1%; Score 7; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSLLLL 181
Db 2 APSLLLL 8

RESULT 11
US-09-461-325-484
; Sequence 484, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16

; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-484

Query Match 3.1%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 24 SLLLLLP 30

RESULT 12
US-10-012-542-484
; Sequence 484, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-012-542-484

Query Match 3.1%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 24 SLLLLLP 30

RESULT 13

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US-10-115-123-484
; Sequence 484, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-484

Query Match          3.1%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 24 SLLLLLP 30
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RESULT 14
US-09-248-796A-26807
; Sequence 26807, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26807
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26807

Query Match          3.1%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 ALLHRL 191
Db 75 ALLHRL 81
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US-09-621-976-3926
; Sequence 3926, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3926
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22..-1
US-09-621-976-3926

Query Match          3.1%; Score 7; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 7 SLLLLLP 13
|||||

Search completed: September 22, 2006, 19:01:54
Job time : 51 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:12:14 ; Search time 169 Seconds
(without alignments)
611.224 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.psp:*
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- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.psp:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	223	100.0	223	4	US-10-665-602-2
2	223	100.0	229	3	US-09-764-893-98
3	223	100.0	229	3	US-09-764-881-101
4	223	100.0	229	3	US-09-764-853-608
5	223	100.0	229	3	US-09-764-898-269
6	223	100.0	229	3	US-09-764-881-101
7	223	100.0	229	4	US-10-073-865-98
8	223	100.0	229	4	US-10-242-747-101
9	187	83.9	223	4	US-10-295-027-422
10	187	83.9	223	4	US-10-295-027-1293
11	187	83.9	223	4	US-10-264-237-2712
12	187	83.9	223	5	US-10-940-431-4
13	187	83.9	231	3	US-09-764-898-198
14	145	65.0	223	4	US-10-257-113-2
15	15	6.7	202	5	US-10-940-431-3
16	9	4.0	157	4	US-10-425-115-351909
17	8	3.6	51	4	US-10-424-599-252112
18	8	3.6	51	4	US-10-437-963-124573
19	8	3.6	55	4	US-10-437-963-141814
20	8	3.6	55	4	US-10-425-115-249327
21	8	3.6	85	4	US-10-425-115-267412
22	8	3.6	105	4	US-10-437-963-180148
23	8	3.6	123	4	US-10-437-963-138083
24	8	3.6	149	6	US-11-096-568A-2904
25	8	3.6	158	6	US-11-097-143-32931
26	8	3.6	170	4	US-10-767-701-58031
27	8	3.6	180	3	US-09-860-670-131

Sequence 131, Appl
Sequence 500, Appl
Sequence 2903, Ap
Sequence 2905, Ap
Sequence 114262, A
Sequence 64569, A
Sequence 68806, A
Sequence 19804, A
Sequence 19803, A
Sequence 335408, A
Sequence 19802, A
Sequence 202387, A
Sequence 63855, A
Sequence 1, Appl
Sequence 54210, A
Sequence 6, Appl
Sequence 25, Appl
Sequence 25, Appl

28 8 3.6 180 4 US-10-227-646-131
29 8 3.6 180 4 US-10-242-355-500
30 8 3.6 209 6 US-11-096-568A-2903
31 8 3.6 209 6 US-11-096-568A-2905
32 8 3.6 349 4 US-10-437-963-114262
33 8 3.6 575 4 US-10-425-114-64569
34 8 3.6 575 4 US-10-425-114-68806
35 8 3.6 619 6 US-11-096-568A-19804
36 8 3.6 668 6 US-11-096-568A-19803
37 8 3.6 720 4 US-10-425-115-335408
38 8 3.6 720 6 US-11-096-568A-19802
39 8 3.6 721 4 US-10-437-963-202387
40 8 3.6 737 4 US-10-425-114-63855
41 8 3.6 1230 5 US-10-416-456A-1
42 8 3.6 1253 5 US-10-450-763-54210
43 8 3.6 1718 4 US-10-415-188-6
44 8 3.6 2524 4 US-10-190-115-25
45 8 3.6 2524 4 US-10-369-072-25

ALIGNMENTS

RESULT 1

US-10-665-602-2
; Sequence 2, Application US/10665602
; Publication No. US20040086967A1
; GENERAL INFORMATION:
; APPLICANT: Meisner, Paul S.
; Coleman, Timothy A.
; TITLE OF INVENTION: Human Cryptin Growth Factor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,602
; FILING DATE: 22-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/393,023A
; FILING DATE: 09-SEP-1999
; APPLICATION NUMBER: US 08/471,371
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marks, Michelle S.
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PF2000D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-602-2

Query Match 100.0%; Score 223; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.4e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 60
Db 1 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 60
Qy 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 120
Db 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 120
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180
Db 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGRPLGLHRL 223
Db 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGRPLGLHRL 223

RESULT 2
US-09-764-893-98
; Sequence 98, Application US/09764893
; Publication No. US20020086330A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P209
; CURRENT APPLICATION NUMBER: US/09/764,893
; CURRENT FILING DATE: 2001-01-19
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-893-98

Query Match 100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 60
Db 7 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 66
Qy 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGRPLGLHRL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGRPLGLHRL 229

RESULT 3
US-09-764-881-101
; Sequence 101, Application US/09764881
; Publication No. US2002008621A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881

; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-101

Query Match 100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 60
Db 7 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 66
Qy 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 180
Db 127 SECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGRPLGLHRL 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLQRRPCGRPLGLHRL 229

RESULT 4
US-09-764-853-608
; Sequence 608, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 608
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-608

Query Match 100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 60
Db 7 MTRHHVRLFTVSLALQIINLNGSYQREKHNGRGEVTKVATQKHROSPLNWTSSHFGE 66
Qy 61 VTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGTCTVLGSCFVCPAHFTGRYCEHDQRR 120

Db 67 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180
Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPGLGHLR 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPGLGHLR 229

RESULT 5

US-09-764-898-269
; Sequence 269, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 269
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-269

Query Match 100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKNGRGVTKVATQKHQSPLNWTSSHFGE 60
Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKNGRGVTKVATQKHQSPLNWTSSHFGE 66
Qy 61 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180
Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPGLGHLR 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPGLGHLR 229

RESULT 6

US-09-764-881-101
; Sequence 101, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 101

LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-101

Query Match 100.0%; Score 223; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKNGRGVTKVATQKHQSPLNWTSSHFGE 60
Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKNGRGVTKVATQKHQSPLNWTSSHFGE 66
Qy 61 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180
Db 127 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 186
Qy 181 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPGLGHLR 223
Db 187 LLPCALLHRLRPDAPAHPRSLVPSVLRERRPCGRPGLGHLR 229

RESULT 7

US-10-073-865-98
; Sequence 98, Application US/10073865
; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P209C1
; CURRENT APPLICATION NUMBER: US/10/073,865
; CURRENT FILING DATE: 2002-02-14
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 98
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-073-865-98

Query Match 100.0%; Score 223; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTRHHVRLFTVSLALQIINLGNYSQREKNGRGVTKVATQKHQSPLNWTSSHFGE 60
Db 7 MTRHHVRLFTVSLALQIINLGNYSQREKNGRGVTKVATQKHQSPLNWTSSHFGE 66
Qy 61 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
Db 67 VTGSAEGWGPEEPLPYSAFEGEGASARPRCCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
Qy 121 SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGAPSLLL 180

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Db      127  SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGGAPSLLL 186

Qy      181  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 223
|||||
Db      187  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 229
|||||

RESULT 8
US-10-242-747-101
; Sequence 101, Application US/10242747
; Publication No. US20040005577A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ07C1
; CURRENT APPLICATION NUMBER: US/10/242,747
; CURRENT FILING DATE: 2002-09-13
; PRIOR FILING DATE: 09/764,881
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2000-01-31
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-747-101

Query Match      100.0%; Score 223; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.5e-196;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGVTKVATQKHQSPLNWTSSHFGE 60
|||||
Db      7  MTRHHVRLFTVSLALQIINLGNISYQREKHNGRGVTKVATQKHQSPLNWTSSHFGE 66
|||||

Qy      61  VTGSAEGWGPEELPYSRAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 120
|||||
Db      67  VTGSAEGWGPEELPYSRAFEGEGASAPRCRNGGTCVLGSCFVCPAHFTGRYCEHDQRR 126
|||||

Qy      121  SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGGAPSLLL 180
|||||
Db      127  SECAGLEHGAWTLRACHLCRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPSAGGAPSLLL 186
|||||

Qy      181  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 223
|||||
Db      187  LLPCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGRPGGLGHL 229
|||||

```

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RESULT 9
US-10-295-027-422
; Sequence 422, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nacasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2000-09-15
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-15
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-21
; PRIOR FILING DATE: 2001-11-29
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2002-01-08
; PRIOR FILING DATE: 2002-01-10
; PRIOR FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 422
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-422

Query Match      83.9%; Score 187; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-163;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      37  EYTKVATQKHQSPLNWTSSHFGEVTSAGWGPEELPYSRAFEGEGASAPRCRNGGT 96
|||||
Db      37  EYTKVATQKHQSPLNWTSSHFGEVTSAGWGPEELPYSRAFEGEGASAPRCRNGGT 96
|||||

Qy      97  CVLGSEFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
|||||
Db      97  CVLGSEFCVCPAHFTGRYCEHDQRRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
|||||

Qy      157  CDPKDFLASHAHGSPSAGGAPSLLLLPCCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGR 216
|||||
Db      157  CDPKDFLASHAHGSPSAGGAPSLLLLPCCALLHRLRLPDAPAHPRSLVPSVLQRRRPPCGR 216
|||||

Qy      217  PGLGHL 223
|||||
Db      217  PGLGHL 223
|||||

RESULT 10

```

```

; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2712
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-237-2712

Query Match      83.9%; Score 187; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-163;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37  EVTKVATQKHRSPLNWTSSHFGEVGTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGT 96
DB      37  EVTKVATQKHRSPLNWTSSHFGEVGTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGT 96

QY      97  CVLGSGFCVCPAFTGRYCEHDQRSSCGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
DB      97  CVLGSGFCVCPAFTGRYCEHDQRSSCGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

QY      157  CDPKDFLASHAGPSAGGAPSLLLLLPCALLHLLRPDAPAHPRSLVPSVLQRRRPPCGR 216
DB      157  CDPKDFLASHAGPSAGGAPSLLLLLPCALLHLLRPDAPAHPRSLVPSVLQRRRPPCGR 216

QY      217  PGLGHRLL 223
DB      217  PGLGHRLL 223

RESULT 12
US-10-940-431-4
; Sequence 4, Application US/10940431
; Publication No. US20050208045A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie
; APPLICANT: Harrison, Craig A.
; APPLICANT: Gray, Peter C.
; TITLE OF INVENTION: Cripto Antagonism of Activin and TGF- (
; TITLE OF INVENTION: Signaling
; FILE REFERENCE: D6525
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: 60/503,046
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Macintosh Os 10
; SEQ ID NO 4
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of human Criptic protein
US-10-940-431-4

Query Match      83.9%; Score 187; DB 5; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.8e-163;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      37  EVTKVATQKHRSPLNWTSSHFGEVGTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGT 96
DB      37  EVTKVATQKHRSPLNWTSSHFGEVGTGSAEGWGPEEPLPYSRAFGEGASARPRCCRNNGT 96

QY      97  CVLGSGFCVCPAFTGRYCEHDQRSSCGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156

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Db 97 CVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Qy 157 CDPKDFLASHAHGSPAGGAPSLLLLPALLHRLLRDPADPAHPRSLVPSVQLQRRPCGR 216
Db 157 CDPKDFLASHAHGSPAGGAPSLLLLPALLHRLLRDPADPAHPRSLVPSVQLQRRPCGR 216
Qy 217 PGLGHRL 223
Db 217 PGLGHRL 223

RESULT 13

US-09-764-898-198
; Sequence 198, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (44)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-198

Query Match 83.9%; Score 187; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.9e-163; Indels 0; Gaps 0;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 EVTKVATQKHKRQSPLNWTSSTSHFGVGTGSAEGWGPEEPLPYSAFGEASARPCCRNGGT 96
Db 45 EVTKVATQKHKRQSPLNWTSSTSHFGVGTGSAEGWGPEEPLPYSAFGEASARPCCRNGGT 104
Qy 97 CVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 156
Db 105 CVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHLCRCIFGALHCLPLQTPDR 164
Qy 157 CDPKDFLASHAHGSPAGGAPSLLLLPALLHRLLRDPADPAHPRSLVPSVQLQRRPCGR 216
Db 165 CDPKDFLASHAHGSPAGGAPSLLLLPALLHRLLRDPADPAHPRSLVPSVQLQRRPCGR 224
Qy 217 PGLGHRL 223
Db 225 PGLGHRL 231

RESULT 14

US-10-257-113-2
; Sequence 2, Application US/10257113
; Publication No. US20030207293A1
; GENERAL INFORMATION:
; APPLICANT: DUCKER, KLAUS
; TITLE OF INVENTION: CRYPTIC-LIKE SECRETED PROTEIN
; FILE REFERENCE: MERCK-2519
; CURRENT APPLICATION NUMBER: US/10/257,113
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: EP 00107142.2
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 223
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-257-113-2

Query Match 65.0%; Score 145; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 7.7e-125;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 AFGEGASARPCRCRNGGTCVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHL 138
Db 79 AFGEGASARPCRCRNGGTCVLGSCVCPAHTGTCYCEHQRSECGALEHGAWTLRACHL 138
Qy 139 CRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGGAPSLLLLPALLHRLLRDPADPAH 198
Db 139 CRCIFGALHCLPLQTPDRCDPKDFLASHAHGSPAGGAPSLLLLPALLHRLLRDPADPAH 198
Qy 199 PRSLVPSVQLQRRPCGRPGLGHRL 223
Db 199 PRSLVPSVQLQRRPCGRPGLGHRL 223

RESULT 15

US-10-940-431-3
; Sequence 3, Application US/10940431
; Publication No. US20050208045A1
; GENERAL INFORMATION:
; APPLICANT: Vale, Wylie
; APPLICANT: Harrison, Craig A.
; APPLICANT: Gray, Peter C.
; TITLE OF INVENTION: Crypto Antagonism of Activin and TGF-
; TITLE OF INVENTION: Signaling
; FILE REFERENCE: D6525
; CURRENT APPLICATION NUMBER: US/10/940,431
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: 60/503,046
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 3
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence of mouse Criptic protein
US-10-940-431-3

Query Match 6.7%; Score 15; DB 5; Length 202;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NGGTCVLGSCVCPA 107
Db 101 NGGTCVLGSCVCPA 115

Search completed: September 22, 2006, 19:15:43
Job time : 171 secs

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OM protein - protein search, using sw model

Run on: September 22, 2006, 19:13:04 ; Search time 34 seconds
(without alignment)
466.741 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRHVRHLLFTVSLALQII.....PSVLQRRRRCGRGLGHL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 260401 seqs, 71162236 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1506

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.6	105	6	US-10-449-902-29843
2	8	3.6	105	6	US-10-449-902-31212
3	8	3.6	105	6	US-10-449-902-32435
4	8	3.6	112	6	US-10-449-902-49548
5	8	3.6	149	6	US-10-953-349-18763
6	8	3.6	186	6	US-10-449-902-41657
7	8	3.6	209	6	US-10-953-349-18762
8	8	3.6	349	6	US-10-449-902-49942
9	8	3.6	349	6	US-10-449-902-50970
10	8	3.6	721	6	US-10-449-902-45561
11	8	3.6	721	6	US-10-449-902-48415
12	8	3.6	788	6	US-10-530-187-275
13	8	3.6	880	6	US-10-449-902-41116
14	7	3.1	50	7	US-11-155-989-716
15	7	3.1	51	7	US-11-155-989-715
16	7	3.1	52	7	US-11-155-989-713
17	7	3.1	52	7	US-11-155-989-714
18	7	3.1	73	6	US-10-449-902-38162
19	7	3.1	107	6	US-10-953-349-12304
20	7	3.1	109	7	US-11-155-989-805
21	7	3.1	112	7	US-11-155-989-462
22	7	3.1	119	6	US-10-196-749-140
23	7	3.1	119	6	US-10-525-116-1106
24	7	3.1	119	7	US-11-101-316-26
25	7	3.1	119	7	US-11-376-673-26

26	7	3.1	119	7	US-11-407-991-2	Sequence 2, Appli
27	7	3.1	126	7	US-11-056-355B-2346	Sequence 2346, Ap
28	7	3.1	151	6	US-10-953-349-14739	Sequence 14739, A
29	7	3.1	151	7	US-11-056-355B-60155	Sequence 60155, A
30	7	3.1	156	7	US-11-337-533-272	Sequence 272, App
31	7	3.1	179	7	US-11-174-307B-5464	Sequence 5464, App
32	7	3.1	179	7	US-11-360-459-154	Sequence 154, App
33	7	3.1	186	6	US-10-953-349-14738	Sequence 14738, A
34	7	3.1	186	7	US-11-056-355B-60154	Sequence 60154, A
35	7	3.1	194	6	US-10-449-902-46396	Sequence 46396, A
36	7	3.1	239	7	US-11-056-355B-96514	Sequence 96514, A
37	7	3.1	254	7	US-11-030-653-18	Sequence 18, Appl
38	7	3.1	256	7	US-11-056-355B-14550	Sequence 14550, A
39	7	3.1	273	7	US-11-330-403-18828	Sequence 18828, A
40	7	3.1	294	6	US-10-953-349-26719	Sequence 26719, A
41	7	3.1	295	6	US-10-449-902-47068	Sequence 47068, A
42	7	3.1	295	6	US-10-449-902-48050	Sequence 48050, A
43	7	3.1	295	6	US-10-449-902-53119	Sequence 53119, A
44	7	3.1	298	6	US-10-953-349-36004	Sequence 36004, A
45	7	3.1	326	6	US-10-540-898-169	Sequence 169, App

ALIGNMENTS

RESULT 1

US-10-449-902-29843
; Sequence 29843, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29843
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29843

Query Match 3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLILLLP 183
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Db 42 PSLILLLP 49

RESULT 2

US-10-449-902-31212
; Sequence 31212, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31212
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-31212

Query Match          3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLLP 183
Db 73 PSLLLLLP 80

RESULT 3
US-10-449-902-32435
; Sequence 32435, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32435
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32435

Query Match          3.6%; Score 8; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 PSLLLLLP 183
Db 73 PSLLLLLP 80

RESULT 4
US-10-449-902-49548
; Sequence 49548, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 49548
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49548

Query Match          3.6%; Score 8; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSLLLLL 182
Db 45 APSLLLLL 52

RESULT 5
US-10-953-349-18763
; Sequence 18763, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18763
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18763

Query Match          3.6%; Score 8; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LFTVSLAL 17
Db 103 LFTVSLAL 110

RESULT 6
US-10-449-902-41657
; Sequence 41657, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41657
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41657

Query Match          3.6%; Score 8; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 ALLHRLLR 192
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Db      146 ALLHRLLR 153
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RESULT 7
US-10-953-349-18762
; Sequence 18762, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18762
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18762

Query Match      3.6%; Score 8; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LFTVSLAL 17
|||||
Db      163 LFTVSLAL 170

RESULT 8
US-10-449-902-49942
; Sequence 49942, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49942
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49942

Query Match      3.6%; Score 8; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      176 PSLLLLLP 183
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Db      4 PSLLLLLP 11

RESULT 9
US-10-449-902-50970
; Sequence 50970, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
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; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50970
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50970

Query Match      3.6%; Score 8; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      176 PSLLLLLP 183
|||||
Db      4 PSLLLLLP 11

RESULT 10
US-10-449-902-45561
; Sequence 45561, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45561
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45561

Query Match      3.6%; Score 8; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      185 ALLHRLLR 192
|||||
Db      107 ALLHRLLR 114

RESULT 11
US-10-449-902-48415
; Sequence 48415, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
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; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48415
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48415

Query Match          3.6%; Score 8; DB 6; Length 721;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 ALLHRLR 192
Db 107 ALLHRLR 114

RESULT 12
US-10-530-187-275
; Sequence 275, Application US/10530187
; Publication No. US20060183120A1
; GENERAL INFORMATION:
; APPLICANT: THE, Bin Tean
; APPLICANT: TAKAHASHI, Masayuki
; TITLE OF INVENTION: Molecular Subclassification of Kidney Tumors and the Discovery of
; TITLE OF INVENTION: New Diagnostic Markers
; FILE REFERENCE: 28927-0014
; CURRENT APPLICATION NUMBER: US/10/530,187
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031476
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US 60/415,775
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 788
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-530-187-275

Query Match          3.6%; Score 8; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 APSLLLLL 182
Db 12 APSLLLLL 19

RESULT 13
US-10-449-902-41116
; Sequence 41116, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41116
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41116

Query Match          3.1%; Score 7; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 CGRPGGLG 220
Db 38 CGRPGGLG 44

RESULT 15
US-11-155-989-715
; Sequence 715, Application US/11155989
; Publication No. US20060177831A1
; GENERAL INFORMATION:
; APPLICANT: Stemmer, Willem P. C.
; APPLICANT: Perlroth, D. Victor
; APPLICANT: Satyal, Sanjeev
; APPLICANT: Alba, Benjamin M.
; APPLICANT: Bakker, Alice
; APPLICANT: Duguay, Amy N.
; APPLICANT: Liu, Qiang
; APPLICANT: Silverman, Joshua
; APPLICANT: Smith, Richard
; APPLICANT: Avidia Research Institute
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; TITLE OF INVENTION: c-Met Kinase Binding Proteins
; FILE REFERENCE: 022013-001410US
; CURRENT APPLICATION NUMBER: US/11/155,989
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/871,602
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 10/957,351
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 925
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 715
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: c-Met-binding family 9 (Fam9)
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (17)...(17)
; OTHER INFORMATION: Xaa = any amino acid
US-11-155-989-715

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Query Match      3.1%; Score 7; DB 7; Length 51;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      214  CGRPGLG 220
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Db       38  CGRPGLG 44

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Job time : 36 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 22, 2006, 18:55:33 ; Search time 38 Seconds
(without alignments)

564.640 Million cell updates/sec

Title: US-10-665-602-2

Perfect score: 223

Sequence: 1 MTRHHVRLFTVSLAQII.....PSVLQRRRPGRGLGRL 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_80:*
1: Pirl1.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.6	162	2 A72770	hypothetical prote
2	8	3.6	859	2 S61246	origin-binding pro
3	8	3.6	2524	2 A35844	Xotch protein - Af
4	7	3.1	22	2 P11333	Ig heavy chain DJ
5	7	3.1	52	2 AF0293	hypothetical prote
6	7	3.1	76	2 AF1928	hypothetical prote
7	7	3.1	104	2 A10775	conserved hypothet
8	7	3.1	109	2 B70037	hypothetical prote
9	7	3.1	195	2 B83506	hypothetical prote
10	7	3.1	198	2 T26708	hypothetical prote
11	7	3.1	249	2 P87313	hydroxyacylglutath
12	7	3.1	264	2 F64896	probable membrane
13	7	3.1	264	2 H85733	probable transport
14	7	3.1	264	2 G90884	probable transport
15	7	3.1	269	2 E95999	probable methyl-tr
16	7	3.1	291	2 I39737	hypothetical prote
17	7	3.1	291	2 T23595	hypothetical prote
18	7	3.1	293	2 B64800	probable multiple
19	7	3.1	293	2 B90865	hypothetical prote
20	7	3.1	293	2 G85753	hypothetical prote
21	7	3.1	294	2 B71256	conserved hypothet
22	7	3.1	296	2 T04703	hypothetical prote
23	7	3.1	304	2 A33274	insulin-like growt
24	7	3.1	305	2 JN0508	insulin-like growt
25	7	3.1	305	2 I48601	insulin-like growt
26	7	3.1	312	2 I78664	hypothetical prote
27	7	3.1	312	2 H91237	hypothetical prote
28	7	3.1	312	2 D86085	hypothetical prote
29	7	3.1	322	2 HB7111	probable transcrip

30	7	3.1	333	1 HLHUCB	T-cell surface gly
31	7	3.1	352	2 T06935	photosystem II pro
32	7	3.1	366	1 A40056	inhibin alpha chai
33	7	3.1	374	2 B96737	hypothetical prote
34	7	3.1	380	2 JC2579	manganese peroxida
35	7	3.1	385	2 T24324	hypothetical prote
36	7	3.1	390	2 F86461	F14M2.7 protein -
37	7	3.1	411	2 A75479	citrate synthase -
38	7	3.1	421	2 T35205	citrate synthase-1
39	7	3.1	434	2 S25958	gene coxI intron 4
40	7	3.1	446	2 T10103	cytochrome-c oxida
41	7	3.1	471	2 T43803	cytochrome-c oxida
42	7	3.1	508	2 S74200	cytochrome-c oxida
43	7	3.1	510	2 H87320	conserved hypothet
44	7	3.1	513	1 ODHU1	cytochrome-c oxida
45	7	3.1	514	2 S29810	monoamine transpor

ALIGNMENTS

RESULT 1

A72770

hypothetical protein APE0148 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Sep-2000

C:Accession: A72770

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: A72770

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-162 <KAW>

A:Cross-references: UNIPARC:UPI000005DA13; DDBJ:AP0000058; NID:G5103398; PIDN:BAA79059.1;

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0148

C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0024

Query Match	3.6%	Score 8;	DB 2;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 3.8;		
Matches	8;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy 14 SLALQIIN 21

Db 4 SLALQIIN 11

RESULT 2

S61246

origin-binding protein - bovine herpesvirus 1

C:Species: bovine herpesvirus 1

C>Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004

C:Accession: S61246

R:Vicek, C.; Benes, V.; Lu, Z.; Kutish, G.F.; Paces, V.; Rock, D.; Letchworth, G.J.; Sch

submitted to the EMBL Data Library, January 1995

A:Description: Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus

A:Reference number: S61233

A:Accession: S61246

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-859 <VLC>

A:Cross-references: UNIPROT:P52377; UNIPARC:UPI0000130B97; EMBL:Z48053; NID:g971311; PID:

C:Superfamily: varicella-zoster virus gene 51 protein

Query Match	3.6%	Score 8;	DB 2;	Length 859;
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Best Local Similarity	100.0%;	Pred. No. 15;		
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Matches	8;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy 185 ALLHRLLR 192

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Db      198 ALLHRLUR 205
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RESULT 3
A35844
Xotch protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 05-Oct-2004
C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
A;Accession: A35844
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2524 <COF>
A;Cross-references: UNIPARC:UPI000004F253
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: transmembrane protein
F;146-177/Domain: EGF homology <EGF1>
F;184-215/Domain: EGF homology <EGF1>
F;222-254/Domain: EGF homology <EGF>
F;456-487/Domain: EGF homology <EGF2>
F;757-788/Domain: EGF homology <EGF3>
F;1025-1056/Domain: EGF homology <EGX3>
F;1924-1956/Domain: ankyrin repeat homology <AN1>
F;1957-1989/Domain: ankyrin repeat homology <AN2>
F;1991-2023/Domain: ankyrin repeat homology <AN3>
F;2024-2056/Domain: ankyrin repeat homology <AN4>
F;2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match      3.6%; Score 8; DB 2; Length 2524;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      91 CRNGGTCV 98
|||||
Db      266 CRNGGTCV 273

RESULT 4
PH1333
Ig heavy chain DJ region (clone C238-133) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1333
R;Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1333
A;Molecule type: DNA
A;Residues: 1-22 <WAS>
A;Cross-references: UNIPARC:UPI000017C236
C;Keywords: heterotetramer; immunoglobulin

Query Match      3.1%; Score 7; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      177 SLLLLLP 183
|||||
Db      8 SLLLLLP 14

RESULT 5
AF0293
hypothetical protein YP02405 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF0293

```

```

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0293
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-52 <KUR>
A;Cross-references: UNIPROT:Q8ZDY9; UNIPARC:UPI00000CD90A; GB:AL590842; PIDN:CAC91210.1;
C;Genetics:
A;Gene: YP02405

Query Match      3.1%; Score 7; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      177 SLLLLLP 183
|||||
Db      36 SLLLLLP 42

RESULT 6
AF1928
hypothetical protein asl0977 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF1928
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF1928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-76 <KUR>
A;Cross-references: UNIPROT:Q8YV74; UNIPARC:UPI00000CDF33; GB:BA000019; PIDN:BA072934.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl0977

Query Match      3.1%; Score 7; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      178 LLLLLLP 184
|||||
Db      8 LLLLLLP 14

RESULT 7
AI0775
conserved hypothetical protein yohN [imported] - Salmonella enterica subsp. enterica sero
C;Species: Salmonella enterica subsp. enterica serovar typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0775
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, F.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0775
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 <PAR>
A;Cross-references: UNIPARC:UPI0000059BFD; GB:AL513382; PIDN:CAD02527.1; PID:gl6503388;
C;Genetics:

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Query Match 3.1%; Score 7; DB 2; Length 195;

C;Accession: F64896
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64896
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-264 <BLAT>
A;Cross-references: UNIPROT:P77505; UNIPARC:UPI000013A92F; GB:AE000241; GB:U00096; NID:8
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: spermidine/putrescine transport system permease protein potI
C;Keywords: inner membrane; transmembrane protein
F;17-33/Domain: transmembrane #status predicted <TM1>
F;71-87/Domain: transmembrane #status predicted <TM2>
F;100-116/Domain: transmembrane #status predicted <TM3>
F;133-149/Domain: transmembrane #status predicted <TM4>
F;186-202/Domain: transmembrane #status predicted <TM5>
F;237-253/Domain: transmembrane #status predicted <TM6>

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Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 102 SLLLLLP 108
|||||
RESULT 13
H85733
probable transport system permease protein Z2276 [imported] - Escherichia coli (strain C
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85733
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <STO>
A;Cross-references: UNIPROT:Q8X9W4; UNIPARC:UPI000000D0789; GB:AE005174; NID:g12515259; F
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2276
C;Superfamily: spermidine/putrescine transport system permease protein potI

Query Match 3.1%; Score 7; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 102 SLLLLLP 108
|||||
RESULT 14
G90884
probable transport system permease protein ECs2047 [imported] - Escherichia coli (strain
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G90884
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuwara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90884
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-264 <HAY>
A;Cross-references: UNIPROT:Q8X9W4; UNIPARC:UPI000000D0789; GB:BA000007; PIDN:BA035470.1;
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs2047
C;Superfamily: spermidine/putrescine transport system permease protein potI

Query Match 3.1%; Score 7; DB 2; Length 264;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 SLLLLLP 183
Db 102 SLLLLLP 108
|||||
RESULT 15
E95999
probable methyl-transferase, S-Adenosyl-L-methionine (SAM)-MTase protein [imported] - Shi
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 12-Jul-2004
C;Accession: E95999
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-269 <KUR>
A;Cross-references: UNIPROT:Q92U77; UNIPARC:UPI00000D4790; GB:AL591985; PIDN:CAC49661.1;
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Punler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpfeil, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaul, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB21433
A;Genome: plasmid
C;Superfamily: spore germination protein C2

Query Match 3.1%; Score 7; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 190 LLRPDAP 196
Db 183 LLRPDAP 189
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Search completed: September 22, 2006, 19:01:00
Job time : 41 secs